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CM protein - protein search, using sw model

Run on: November 10, 2003, 06:16:09 ; Search time 446 Seconds
(without alignments)
95.887 Million cell updates/sec

Title: US-09-503-387-9
Perfect score: 1304
Sequence: 1 QSGPLPKPSLQAIPLSSILVPL... SPKESDSPAGPARQYITKGN 249
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 644079 seqs, 171749292 residues
Total number of hits satisfying chosen parameters: 644079
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA: *
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2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep: *
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUBCOMB.pep: *
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Nc.	Score	Query Match Length	DB ID	Description
1	1304	249	9	US-09-832-312-9 Sequence 9, Appli
2	1304	319	9	US-09-832-312-5 Sequence 5, Appli
3	1304	339	9	US-09-832-312-3 Sequence 3, Appli
4	1304	339	15	US-10-157-031-387 Sequence 387, Appli
5	1304	100.0	369	12 US-10-446-826-37 Sequence 37, Appli
6	1300	99.7	339	9 JS-09-832-312-34 Sequence 34, Appli
7	1300	99.7	339	9 JS-C9-832-312-36 Sequence 36, Appli
8	1300	99.7	339	9 US-09-832-312-38 Sequence 38, Appli
9	1300	99.7	339	9 US-09-832-312-40 Sequence 40, Appli
10	1277	37.9	12	US-10-446-826-5 Sequence 5, Appli
11	895.5	68.7	267	9 US-09-832-312-19 Sequence 19, Appli
12	895.5	68.7	292	9 US-09-832-312-18 Sequence 18, Appli
13	895.5	68.7	313	9 US-09-832-312-16 Sequence 16, Appli
14	895.5	68.7	313	9 US-09-832-312-48 Sequence 48, Appli
15	891.5	68.4	313	9 US-09-832-312-42 Sequence 42, Appli

RESULT 1
US-09-832-312-9
; Sequence 9, Application US/09832312
; Patent No. JJS20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Bustfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-9

Query Match Score 100.0%; Score i304; DB 9; Length: 249;
Best Local Similarity 100.0%; Pred. No. 4.8e-104;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 44, Appli
Sequence 46, Appli
Sequence 50, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 36, Appli
Sequence 92, Appli
Sequence 12, Appli
Sequence 20, Appli
Sequence 22, Appli
Sequence 20, Appli
Sequence 2, Appli
Sequence 14, Appli
Sequence 16, Appli
Sequence 16, Appli
Sequence 14, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 20, Appli
Sequence 10, Appli
Sequence 10, Appli

1 QSGPLPKPSLQAIPLSSILVPLKEPTI,RCQGPPGVLDYRLEKCSSSRYRCDOAVLFIPAMKR 60
1 QSGPLPKPSLQAIPLSSILVPLKEPTI,RCQGPPGVLDYRLEKCSSSRYRCDOAVLFIPAMKR 60
61 SLAGRYSRSYQNGSLSLPSDQELVATGFAKPLSLAQPGPAVSSGGDVTLQQCTRYGF 120
61 SLAGRYSRSYQNGSLSLPSDQELVATGFAKPLSLAQPGPAVSSGGDVTLQQCTRYGF 120

RESULT 2
JS-09-832-312-5
; Sequence 5, Application 'US/39832312
; Patent No. US2001C049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/C9/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/613,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: C9/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: C9/454,924
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 319
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-5

Query Match 100.0%; Score 1304; DB 9; Length 319;
Best Local Similarity 100.0%; Pred. No. 6.6e-104; Mismatches 0; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
; OSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
Db 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 80

QY 61 SLAGRYRCYQNGSJWSLPSDQELVATGVFAKPSLSAQPGPAVSSGGDNTQCQTRYGF 120
; SLAGRYRCYQNGSJWSLPSDQELVATGVFAKPSLSAQPGPAVSSGGDNTQCQTRYGF 120
Db 81 SLAGRYRCYQNGSJWSLPSDQELVATGVFAKPSLSAQPGPAVSSGGDNTQCQTRYGF 140

QY 121 DQFALYKEGDAPYKPERWYRASFPITTAHSGTYRCYSFSSRDPYLWSAPSDELE 180
; DQFALYKEGDAPYKPERWYRASFPITTAHSGTYRCYSFSSRDPYLWSAPSDELE 200

QY 181 VVTGTSTVPSRLPTEPPSSVAEFSSEATAELTVSFINKVFTTETRSRITSSPKESDSPAGP 240
; VVTGTSTVPSRLPTEPPSSVAEFSSEATAELTVSFINKVFTTETRSRITSSPKESDSPAGP 260

QY 241 ARQYYTKGN 249
Db 261 ARQYYTKGN 269

RESULT 3
JS-09-832-312-3
; Sequence 3, Application US/09832312
; Patent No. US2001049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312

Query Match 100.0%; Score 1304; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-104; Mismatches 0; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
; QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
Db 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 80

QY 61 SLAGRYRCYQNGSJWSLPSDQELVATGVFAKPSLSAQPGPAVSSGGDNTQCQTRYGF 120
; SLAGRYRCYQNGSJWSLPSDQELVATGVFAKPSLSAQPGPAVSSGGDNTQCQTRYGF 120
Db 81 SLAGRYRCYQNGSJWSLPSDQELVATGVFAKPSLSAQPGPAVSSGGDNTQCQTRYGF 140

QY 121 DQFALYKEGDAPYKPERWYRASFPITTAHSGTYRCYSFSSRDPYLWSAPSDELE 180
; DQFALYKEGDAPYKPERWYRASFPITTAHSGTYRCYSFSSRDPYLWSAPSDELE 200

QY 181 VVTGTSTVPSRLPTEPPSSVAEFSSEATAELTVSFINKVFTTETRSRITSSPKESDSPAGP 240
; VVTGTSTVPSRLPTEPPSSVAEFSSEATAELTVSFINKVFTTETRSRITSSPKESDSPAGP 260

QY 241 ARQYYTKGN 249
Db 261 ARQYYTKGN 269

RESULT 4
JS-10-157-031-387
; Sequence 387, Application US/10157031
; Publication No. US20030108890A1
; GENERAL INFORMATION:
; APPLICANT: Baranova, A. V.
; APPLICANT: Yankovsky, N. K.
; APPLICANT: Kozlov, A. P.
; APPLICANT: Lobachev, A. V.
; APPLICANT: Krukovskaya, L. L.
; TITLE OF INVENTION: In silico screening for phenotype-associated expressed sequence
; FILE REFERENCE: 2760-103
; CURRENT APPLICATION NUMBER: US/10/157,031
; CURRENT FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 415
; SOFTWARE: Patent version 3.1
; SEQ ID NO 387
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-157-031-387

Query Match 100.0%; Score 1304; DB 15; Length 339;
Best Local Similarity 100.0%; Pred. No. 7.2e-104; Mismatches 0; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
; QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
Db 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVLFIPAMKR 80

RESULT 5
; Sequence 37, Application US/10446826
; Publication No. US20030186885A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOFROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-34

Query Match: 99.7%; Score 1300; DB 9; Length 339;
Best Local Similarity 99.6%; Pred. No. 1.6e-103; Mismatches 0; Indels 0; Gaps 0;
Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYREKLSSRQYDQAVLFIPAMKR 60
Db 21 QSGPLPKPSLQVLPSLVPVTLRCQGPGVLDYREKLSSRQYDQAVLFIPAMKR 80

Qy 61 SLAGRYRCSYONGSLWSPSDQELVATGVFAKPLSAQGPAGVSSGGDVTLQCQTRYGF 120
Db 81 SLAGRYRCSYONGSLWSPSDQELVATGVFAKPLSAQGPAGVSSGGDVTLQCQTRYGF 140

Qy 121 DQFALYKEGDPAPYKPERWYRAFPIITVTAHSGTYRCYSFSSRDPYLWSAPSDELEL 180
Db 141 DQFALYKEGDPAPYKPERWYRAFPIITVTAHSGTYRCYSFSSRDPYLWSAPSDELEL 200

Qy 181 VVTGTTSVTPSRLPTEPPSSVAEFESEATAELTVSFTNKFETTTSRSITSPKESDSPAGP 240
Db 201 VVTGTTSVTPSRLPTEPPSSVAEFESEATAELTVSFTNKFETTTSRSITSPKESDSPAGP 260

Qy 241 AROYYTKGN 249
Db 261 AROYYTKGN 269

RESULT 6
; Sequence 34, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOFROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-34

Query Match: 100.0%; Score 1304; DB 12; Length 369;
Best Local Similarity 100.0%; Pred. No. 8e-104; Mismatches 0; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYREKLSSRQYDQAVLFIPAMKR 60
Db 98 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLDYREKLSSRQYDQAVLFIPAMKR 157

Qy 61 SLAGRYRCSYONGSLWSPSDQELVATGVFAKPLSAQGPAGVSSGGDVTLQCQTRYGF 120
Db 58 SLAGRYRCSYONGSLWSPSDQELVATGVFAKPLSAQGPAGVSSGGDVTLQCQTRYGF 217

Qy 121 DQFALYKEGDPAPYKPERWYRAFPIITVTAHSGTYRCYSFSSRDPYLWSAPSDELEL 180
Db 219 DQFALYKEGDPAPYKPERWYRAFPIITVTAHSGTYRCYSFSSRDPYLWSAPSDELEL 227

Qy 181 VVTGTTSVTPSRLPTEPPSSVAEFESEATAELTVSFTNKFETTTSRSITSPKESDSPAGP 240
Db 278 VVTGTTSVTPSRLPTEPPSSVAEFESEATAELTVSFTNKFETTTSRSITSPKESDSPAGP 337

Qy 241 AROYYTKGN 249
Db 338 AROYYTKGN 346

RESULT 7
; Sequence 36, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOFROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-832-312-34

US-09-832-312-36

Query Match: 99.7%; Score 1300; DB 9; Length: 339;
 Best Local Similarity 99.6%; Pred. No. 1.6e-103;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY  1 QSGPLPKPSIQLPSSVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDCAVLFIPAMKR 60
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    21 QSGPLPKPSIQLPSSVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDCAVLFIPAMKR 80
      ; Sequence 40, Application US/09832312
      ; Patent No. US20010049829A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Busfield et al.
      ; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
      ; FILE REFERENCE: 7853-234
      ; CURRENT APPLICATION NUMBER: US/09/832,312
      ; CURRENT FILING DATE: 2001-04-09
      ; PRIOR APPLICATION NUMBER: 09/610,118
      ; PRIOR FILING DATE: 2000-06-30
      ; PRIOR APPLICATION NUMBER: 09/503,387
      ; PRIOR FILING DATE: 1999-12-06
      ; PRIOR APPLICATION NUMBER: 09/345,468
      ; PRIOR FILING DATE: 1999-06-30
      ; NUMBER OF SEQ ID NOS: 78
      ; SOFTWARE: FastSEQ for Windows Version 3.0
      ; SEQ ID NO 40
      ; LENGTH: 339
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; US-09-832-312-40

QY  121 DQFALYKEGDAPAYKNPERWYRASFPIITVTAHSGTYRCYSFSSRDPYJWSAPSDEL 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 
    141 DQFALYKEGDAPAYKNPERWYRASFPIITVTAHSGTYRCYSFSSRDPYJWSAPSDEL 200
      ; Sequence 40, Application US/09832312
      ; Patent No. US20010049829A1
      ; GENERAL INFORMATION:
      ; APPLICANT: Busfield et al.
      ; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
      ; FILE REFERENCE: 7853-234
      ; CURRENT APPLICATION NUMBER: US/09/832,312
      ; CURRENT FILING DATE: 2001-04-09
      ; PRIOR APPLICATION NUMBER: 09/610,118
      ; PRIOR FILING DATE: 2000-06-30
      ; PRIOR APPLICATION NUMBER: 09/503,387
      ; PRIOR FILING DATE: 1999-12-06
      ; PRIOR APPLICATION NUMBER: 09/345,468
      ; PRIOR FILING DATE: 1999-06-30
      ; NUMBER OF SEQ ID NOS: 78
      ; SOFTWARE: FastSEQ for Windows Version 3.0
      ; SEQ ID NO 40
      ; LENGTH: 339
      ; TYPE: PRT
      ; ORGANISM: Homo sapiens
      ; US-09-832-312-40

QY  1 QSGPLPKPSIQLPSSVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDCAVLFIPAMKR 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 
    21 QSGPLPKPSIQLPSSVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDCAVLFIPAMKR 80
      ; Sequence 5, Application US/10446826
      ; Publication No. US20030186885A1
      ; GENERAL INFORMATION:
      ; APPLICANT: TANDON, NARENDRA N.
      ; APPLICANT: SUN, BING
      ; APPLICANT: NAKAMURA, TAKASHI
      ; APPLICANT: YAMAMOTO, NACOMASA
      ; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
      ; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
      ; FILE REFERENCE: 03459.0026-0000
      ; CURRENT APPLICATION NUMBER: US/10/446,826
      ; CURRENT FILING DATE: 2003-05-29
      ; PRIOR APPLICATION NUMBER: US/09/653,255B
      ; PRIOR FILING DATE: 2000-08-31
      ; PRIOR APPLICATION NUMBER: PCT/US00/23975

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US-09-832-312-36

Query Match: 99.7%; Score 1300; DB 9; Length: 339;
 Best Local Similarity 99.6%; Pred. No. 1.6e-103;
 Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY  1 QSGPLPKPSIQLPSSVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDCAVLFIPAMKR 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| 
    21 QSGPLPKPSIQLPSSVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDCAVLFIPAMKR 80
      ; Sequence 5, Application US/10446826
      ; Publication No. US20030186885A1
      ; GENERAL INFORMATION:
      ; APPLICANT: TANDON, NARENDRA N.
      ; APPLICANT: SUN, BING
      ; APPLICANT: NAKAMURA, TAKASHI
      ; APPLICANT: YAMAMOTO, NACOMASA
      ; TITLE OF INVENTION: PLATELET MEMBRANE GLYCOPROTEIN VI (GPVI) DNA AND
      ; TITLE OF INVENTION: PROTEIN SEQUENCES, AND USES THEREOF
      ; FILE REFERENCE: 03459.0026-0000
      ; CURRENT APPLICATION NUMBER: US/10/446,826
      ; CURRENT FILING DATE: 2003-05-29
      ; PRIOR APPLICATION NUMBER: US/09/653,255B
      ; PRIOR FILING DATE: 2000-08-31
      ; PRIOR APPLICATION NUMBER: PCT/US00/23975

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; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/152,197
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: 60/158,251
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-446-826-5

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Query Match 97.9%; Score 1277; DB 12; Length 339;
Best Local Similarity 98.8%; Pred. No. 1.5e-101; Mismatches 3; Indels 0; Gaps 0;
Matches 246; Conservative 0; Mismatches 3;

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Qy   : QSGPLPKPSLQALPSLVLPEKPTVLRQGPPGVDFYRLEKSSSRYQDQAVLFIPAMKR 60
Db   : 21 QSGPLPKPSLQALPSLVLPEKPTVLRQGPPGVDFYRLEKSSSRYQDQAVLFIPAMKR 80
Qy   : 61 SLAGRYRCSYQNGSLWISLPSDQEELVATGVFAKPLSACQGPAGVSSGGDVTLCQTRYGF 120
Db   : 81 SLAGRYRCSYQNGSLWISLPSDQEELVATGVFAKPLSACQGPAGVSSGGDVTLCQTRYGF 140
Qy   : 121 DQFALYKEGDPAKYKNPERWYRASPIITVTAHSHTYRCYSFSSRDPYLNSAPSDELEL 180
Db   : 141 DQFALYKEGDPAKYKNPERWYRASPIITVTAHSHTYRCYSFSSRDPYLNSAPSDELEL 200
Qy   : 181 VVTGTSVTPSLRPTEPSSVAESEATAELTVSFNKVFTETRSRITSITSPKEDSPAGP 240
Db   : 201 VVTGTSVTPSLRPTEPSSVAESEATAELTVSFNKVFTETRSRITSITSPKEDSPAGP 260
Qy   : 241 ARQYYTKGN 249
Db   : 261 ARQYYTKGN 269

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RESULT 11

US-09-832-312-19

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; Sequence 19, Application US/09832312
; Patent No. US20010049829A1

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; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-832-312-18

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US-09-832-312-18

Query Match 68.7%; Score 895.5; DB 9; Length: 292;
Best Local Similarity 69.9%; Pred. No. 6.7e-69; Mismatches 174; Conservative 18; Mismatches 18; Indels 3; Gaps 1;

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Qy   : 1 QSGPLPKPSLQALPSLVLPEKPTVLRQGPPGVDFYRLEKSSSRYQDQAVLFIPAMKR 60
Db   : 1 QSGPLPKPSLQALPSLVLPEKPTVLRQGPPGVDFYRLEKSSSRYQDQAVLFIPAMKR 60
Qy   : 61 SLAGRYRCSYQNGSLWISLPSDQEELVATGVFAKPLSACQGPAGVSSGGDVTLCQTRYGF 120
Db   : 62 SLAGRYRCSYQNGSLWISLPSDQEELVATGVFAKPLSACQGPAGVSSGGDVTLCQTRYGF 140
Qy   : 121 DQFALYKEGDPAKYKNPERWYRASPIITVTAHSHTYRCYSFSSRDPYLNSAPSDELEL 180
Db   : 122 DQFALYKEGDPAKYKNPERWYRASPIITVTAHSHTYRCYSFSSRDPYLNSAPSDELEL 200
Qy   : 181 VVTGTSVTPSLRPTEPSSVAESEATAELTVSFNKVFTETRSRITSITSPKEDSPAGP 240
Db   : 182 VVTGLSATPSQVPTESFPVTESSRRPSILP---TNKISTTEKPMNITASPEGSLPPIGF 258
Qy   : 241 ARQYYTKGN 249
Db   : 238 AHQHYAKGN 246

```

US-09-832-312-19

Query Match 68.7%; Score 895.5; DB 9; Length 267;
Best Local Similarity 69.9%; Pred. No. 6e-69; Mismatches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

```

Qy   : 1 QSGPLPKPSLQALPSLVLPEKPTVLRQGPPGVDFYRLEKSSSRYQDQAVLFIPAMKR 60
Db   : 22 QSGPLPKPSLQALPSLVLPEKPTVLRQGPPGVDFYRLEKSSSRYQDQAVLFIPAMKR 81
Qy   : 61 SLAGRYRCSYQNGSLWISLPSDQEELVATGVFAKPLSACQGPAGVSSGGDVTLCQTRYGF 120

```

RESULT 13

JS-09-832-312-16

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; Sequence 16, Application US/09832312
; Patent No. US20010049829A1
; GENERAL INFORMATION:
; APPLICANT: Busfield et al.

```

; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 16
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
; JS-09-832-312-16

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7.3e-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

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QY      1 QSGPLPKPSIQLQALPSSILVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
Db      22 QSGPLPKPSIQLQALPSSILVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDQAVLFIPAMKR 81
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QY 61 SLAGRYRCSYQNGSLWSLPSDQELVALTGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 120
Db 82 SNAGRYRCSYQNGSHWSLPSDQELIAATGVYAKPSLSAHPSSAVPQGRDVTJKCSPYSF 141

QY 121 DQFALKKEGDGPAPYKNPERWYRASPIITVTAHSGTYRCYSFSSRDPYLWSAPSCPLEL 180
Db 142 DEFVLYKEGDTGPYKRPEKWYRANFPPIITVTAHSGTYRCYSFSSSPYLWSAPSQPLVLJ 201

QY 181 VVTGTSVTPSLPTEPPSSVAEFSSEATAELTVSFINKVFTETRSRITSITSPKESDSPAGP 240
Db 202 VVTGLSATPSQVPTEESEFPVTESSRRPSILP---TNKISTTEKPMNTASPEGISPPIGF 258

QY 241 ARQYVTKGN 249
Db 259 AHQHYAKGN 267

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7.3e-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

RESULT 15

US-09-832-312-42

; Sequence 42, Application US/09832312

; Patent No. US20010C49829A1

; GENERAL INFORMATION:
; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF
; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312

; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 42
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
; JS-09-832-312-42

RESULT 14

US-09-832-312-48

; Sequence 48, Application US/C9832312

; Patent No. US20010049829A1

; GENERAL INFORMATION:

; APPLICANT: Busfield et al.
; TITLE OF INVENTION: GLYCOPROTEIN VI AND USES THEREOF

; FILE REFERENCE: 7853-234
; CURRENT APPLICATION NUMBER: US/09/832,312
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 09/610,118
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/503,387
; PRIOR FILING DATE: 2000-02-14
; PRIOR APPLICATION NUMBER: 09/454,824
; PRIOR FILING DATE: 1999-12-06
; PRIOR APPLICATION NUMBER: 09/345,468
; PRIOR FILING DATE: 1999-06-30

; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 48
; LENGTH: 313
; TYPE: PRT
; ORGANISM: Mus musculus
; JS-09-832-312-48

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7.3e-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

```
QY      1 QSGPLPKPSIQLQALPSSILVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
Db      22 QSGPLPKPSIQLQALPSSILVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDQAVLFIPAMKR 81
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QY 61 SLAGRYRCSYQNGSLWSLPSDQELVALTGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 120
Db 82 SNAGRYRCSYQNGSHWSLPSDQELIAATGVYAKPSLSAHPSSAVPQGRDVTJKCSPYSF 141

QY 121 DQFALKKEGDGPAPYKNPERWYRASPIITVTAHSGTYRCYSFSSRDPYLWSAPSCPLEL 180
Db 142 DEFVLYKEGDTGPYKRPEKWYRANFPPIITVTAHSGTYRCYSFSSSPYLWSAPSQPLVLJ 201

QY 181 VVTGTSVTPSLPTEPPSSVAEFSSEATAELTVSFINKVFTETRSRITSITSPKESDSPAGP 240
Db 202 VVTGLSATPSQVPTEESEFPVTESSRRPSILP---TNKISTTEKPMNTASPEGISPPIGF 258

QY 241 ARQYVTKGN 249
Db 259 AHQHYAKGN 267

Query Match 68.7%; Score 895.5; DB 9; Length 313;
Best Local Similarity 69.9%; Pred. No. 7.3e-69;
Matches 174; Conservative 18; Mismatches 54; Indels 3; Gaps 1;

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QY      1 QSGPLPKPSIQLQALPSSILVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDQAVLFIPAMKR 60
Db      22 QSGPLPKPSIQLQALPSSILVPLEKPVTLRCQGPPGVLDYRLEKLSSRYQDQAVLFIPAMKR 81
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QY 61 SLAGRYRCSYQNGSLWSLPSDQELVALTGVFAKPSLSAQPGPAVSSGGDVTLQCCTRYGF 120
Db 82 SNAGRYRCSYQNGSHWSLPSDQELIAATGVYAKPSLSAHPSSAVPQGRDVTJKCSPYSF 141

QY 121 DQFALKKEGDGPAPYKNPERWYRASPIITVTAHSGTYRCYSFSSRDPYLWSAPSCPLEL 180
Db 142 DEFVLYKEGDTGPYKRPEKWYRANFPPIITVTAHSGTYRCYSFSSSPYLWSAPSQPLVLJ 201

QY 181 VVTGTSVTPSLPTEPPSSVAEFSSEATAELTVSFINKVFTETRSRITSITSPKESDSPAGP 240
Db 202 VVTGLSATPSQVPTEESEFPVTESSRRPSILP---TNKISTTEKPMNTASPEGISPPIGF 258

QY 241 ARQYVTKGN 249
Db 259 AHQHYAKGN 267

Mon Nov 10 06:30:17 2003

us-09-503-387-9.rapp

Page 7

Search completed: November 10, 2003, 06:28:48
Job time : 446 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.
 OM protein - protein search, using sw mode'
 Run on: November 10, 2003, 06:14:09 ; Search time 41 Seconds
 (without alignments)
 363.974 million cell updates/sec

Title: JS-09-503-387-9
 Perfect score: 1304
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 Searched: 1107863 seqs, 158726573 residues
 Total number of hits satisfying chosen parameters: 1107863
 Minimum DB seq length: 0
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 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	1304	100.0	249	22	AAB61261 Human TANGO 268 ex
2	1304	100.0	249	24	AAB61227 Human TANGO 268 ex
3	1304	100.0	319	22	AAB61257 Human TANGO 268 ex
4	1304	100.0	319	22	AAB49403 Human TANGO 268 ex
5	1304	100.0	319	24	AAB61223 Human TANGO 268 ex
6	1304	100.0	339	22	AAB61255 Human TANGO 268 ex
7	1304	100.0	339	24	AAB61221 Human TANGO 268 ex
8	1304	100.0	369	22	AAY72791 Human GAVI extera
9	1304	100.0	501	24	ABP72518 Immunoglobulin Fc-

RESULT 1
 AAB61261
 ID AAB61261 standard; Protein; 249 AA.
 XX
 AC AAB61261;
 XX
 DT 04-APR-2001 (first entry)
 XX
 DE Human TANGO 268 extracellular domain.
 XX
 KW Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.
 XX
 OS Homo sapiens.
 XX
 PR WO2003100810-A1.
 XX
 PC C4-JAN-2001.
 XX
 PF 30-JUN-2000; 2000WO-US18152.
 XX
 PR 30-JUN-1999; 99US-0345468.
 PR 06-DEC-1999; 99US-0454824.
 PR 14-FEB-2000; 2000US-0503387.
 XX
 (MIL-1) MILLENNIUM PHARM INC.
 XX
 PR Busfield SJ, Villela J, Jardot-Perrus M, Vairchenker W, Gill DS;

Query Match		100.0%	Score 1334; DB 22;	Length 319;	
Best Local Similarity		100.0%;	Pred. No. 3.2e-05;		
Matches 249; Conservative		C;	Mismatches 0;	Indels 0;	Gaps 0
Y	QSGPJPKESQLPSSLVPPLEKPVTRCQGPGVPLYRLEKUSSSRVQDQAVLIPAMKR	60			
Y	QGPLPKPSLQALPSSLVPLEKPVTRCQGPGVPLYRLEKUSSSRVQDQAVLIPAMKR	60			
Y	SLAGRYSQYNGSLWLSLPSDOLEUVATGVFAKPSLSAQPGPAVSSGGDWLCCQ-TRYGF	120			
Y	SLAGRYSQYNGSLWLSLPSDOLEUVATGVFAKPSLSAQPGPAVSSGGDWLCCQ-TRYGF	120			
b	61 SLAGRYSQYNGSLWLSLPSDOLEUVATGVFAKPSLSAQPGPAVSSGGDWLCCQ-TRYGF	60			
b	61 SLAGRYSQYNGSLWLSLPSDOLEUVATGVFAKPSLSAQPGPAVSSGGDWLCCQ-TRYGF	60			
b	121 ECFALVKEGDPAPYKPNPERWYRASPFSEATAELTVSFTNKVFETTSRSITSPKESPAGP	240			
b	121 ECFALVKEGDPAPYKPNPERWYRASPFSEATAELTVSFTNKVFETTSRSITSPKESPAGP	240			
b	181 VVTGTSVTPSLPTEPPSSVAEFPSETAELTVSFTNKVFETTSRSITSPKESPAGP	240			
b	181 VVTGTSVTPSLPTEPPSSVAEFPSETAELTVSFTNKVFETTSRSITSPKESPAGP	240			
y	181 VVTGTSVTPSLPTEPPSSVAEFPSETAELTVSFTNKVFETTSRSITSPKESPAGP	240			
y	241 ARQYVTKGN 249	249			
y	241 ARQYVTKGN 249	249			
xx	RESULT 5				
xx	ABU11223				
xx	D ABU11223 standard; Protein; 319 AA.				
xx	AC				
xx	XX				
xx	DT	(first entry)			
xx	DE	Human TANGO 268 mature protein.			
xx	KW	Human; mouse; variable heavy; VH; antigen; cancer;			
xx	KW	complementarity determining region; TANGO 268; glycoprotein V _H ; GPVI;			
xx	KW	TANGO 268; extracellular matrix; collagen; platelet release;			
xx	KW	proliferation; migration; embryogenesis; inflammation; thrombosis;			
xx	KW	degranulation; thrombocytopenia; antibody; thrombotic disorder;			
xx	KW	cerbral vascular disease; stroke; ischaemia; venous thromboembolism;			
xx	KW	leg swelling; pain; ulceration; pulmonary embolism; coronary disease;			
xx	KW	cardiovascular disease; angina pectoris; myocardial infarction;			
xx	KW	coronary restenosis; atherosclerosis; immunological disorder;			
xx	KW	developmental disorder; embryonic disorder; liver disorder;			
xx	KW	cerbral vascular disease; venous thromboembolism disease.			
xx	OS	Homo sapiens.			
xx	PN	WC200280968-A1.			
xx	PP	17-CCT-2002.			
xx	PP	09-APR-2002; 2002WO-US11122.			
xx	PR	09-APR-2001; 2001US-0829495.			
xx	PA	(MIL-.) MILLENNIUM PHARM INC.			
xx	PI	Busfield SJ, Villeval J, Jandrot-Perrus M, Vainchenker W, Gille DS;			
xx	PI	Qian DM, Kingsbury G;			
xx	DR	KP1; 2003-058477/05.			
xx	RS	Disclosure; Page 211-212; 236pp; English.			
xx	CC	This invention relates to a novel purified antibody comprising a variable heavy (VH) complementarity determining region (CDR1), VH CDR2			
xx	CC	Novel substantially purified antibody immunospecifically binding to TANGO 268 antigen, useful for treating bleeding disorders such as thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis			
xx	PT	-			

CC CQ VH CDR3; C γ variable light (V μ) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 CC VI (GPVI) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC Colilager or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC leukocyte-platelet and platelet-endothelium interactions in
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degranulation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopaenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia), venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc); immunological disorders,
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, Platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 XX create the antibodies of the invention.
 SC Sequence 339 AA:
 Query Match: 100.0%; Score 1304; DB 24; length 319;
 Best Local Similarity 100.0%; Pred. No. 3.2e-105;
 Matches 249; Conservative 0; Mismatches 0; Idents 0; Gaps 0;
 QY 1 QSGPLPKPSLQALPSLVPLEKPVTLRCQGPPGVLYRLEKLSSSRYCDQAVLFPAMKR 60
 2 |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 3 QSGPLPKPSLQALPSLVPLEKPVTLRCQGPPGVLYRLEKLSSSRYCDQAVLFPAMKR 60
 QY 61 SIAGGRYRCSYONGSLWSLPSDQELVATGVFAKPSLSAQPGPAVSS3GDVTLOCO TRYGF 120
 62 |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
 63 SIAGGRYRCSYONGSLWSLPSDQELVATGVFAKPSLSAQPGPAVSS3GDVTLOCO TRYGF 120
 Db 121 DDFALYKEGDPAPYKPERWYRASFPITVTAASGTYRCYSFSSRCPYIWSAPSQDPLEL 180
 122 DDFALYKEGDPAPYKPERWYRASFPITVTAASGTYRCYSFSSRCPYIWSAPSQDPLEL 180
 Cy 181 VWTGTSVTPSRPTEPPSSVAEFSERATEILTVSFTNKVFTETRSRSITSPSKEDSPAGP 240
 182 VWTGTSVTPSRPTEPPSSVAEFSERATEILTVSFTNKVFTETRSRSITSPSKEDSPAGP 240
 Db 181 VWTGTSVTPSRPTEPPSSVAEFSERATEILTVSFTNKVFTETRSRSITSPSKEDSPAGP 240
 QY 242 ARQYTTKGN 249
 243 ARQYTTKGN 249
 D5 244 ARQYTTKGN 249
 XX
 RESULT 5
 AAB61255
 IC AAB61255 standard; protein: 339 AA.
 XX
 AC AAB61255;
 XX
 DE Human TANGO 268 protein.
 XX
 Human; TANGO 268; cardiant; cerebroprotective; cytostatic; anticoagulant;
 KW thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI;
 KW platelet membrane glycoprotein receptor; bleeding disorder;
 KW blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke;
 KW ischaemia; cardiovascular disease; immunological disease; liver disorder;
 KW cancer.
 XX
 Homo sapiens.

AC ABU11221;
 XX
 PN WO200100810-A1.
 XX
 PD 04-JAN-2001.
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 PF 30-JUN-2000; 2000WO-US18152.
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 PR 30-JUN-1999; 99US-0345468.
 PR 06-DEC-1999; 99US-0454824.
 PR 14-FEB-2006; 2000US-0503387.
 XX
 PA (MLL-) MILLENNIUM PHARM INC.
 XX
 PI Busfield SJ, Vilieval J, Jandrot-Perrus M, Vainchencker W, Gili DS;
 PI Qian MD, Kingsbury G;
 XX
 DR WPI; 2001-080877/09.
 CR N-PSDB; AAF29470, AAF29471.
 XX
 PT New genes encoding human platelet-expressed collagen receptor,
 PT glycoprotein VI, and its modulators, useful for preventing, treating
 PT and diagnosing hemorrhagic disorders, thrombotic diseases and
 PT immunological disorders.
 XX
 PS Claim 8; Fig 1A; 227pp; English.
 XX
 PR 09-APR-2002; 2002WO-US11122.
 XX
 PR 09-APR-2002; 2002WO-US11122.
 XX
 PR 17-OCT-2002.
 XX
 PR 09-APR-2002; 2002WO-US11122.
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 PR 09-APR-2002; 2001US-0829495.
 XX
 PR (MLL-) MILLENNIUM PHARM INC.
 XX
 PI Busfield SJ, Vilieval J, Jandrot-Perrus M, Vainchencker W, Gili DS;
 PI Qian DM, Kingsbury G;
 XX
 DR WPI; 2003-058477/05.
 DR P-PSDB; ABX17291, ABX17290.
 XX
 PT Novel substantially purified antibody immunospecifically binding to
 PT TANGO 268 antigen, useful for treating bleeding disorders such as
 PT thrombocytopenia, stroke, ischemia, pulmonary embolism, atherosclerosis
 PT -
 XX
 PS Disclosure; Figure 1; 236pp; English.
 XX
 CC This invention relates to a novel purified antibody comprising a
 CC variable heavy (VH) complementarity determining region (CDR)1, VH CDR2
 CC or VH CDR3; or variable light (VL) CDR1, VL CDR2 or VL CDR3, and
 CC immunospecifically binding to a TANGO 268 (also referred as glycoprotein
 VI (GPVI) antigen. The antibodies of the invention act to decrease or
 CC block TANGO 268 binding to extracellular matrix components, or as a
 CC leukocyte or platelet release and aggregation blocker. The antibodies of
 CC the invention are useful for modulating proliferation, migration,
 CC morphology, differentiation and/or function of megakaryocytes and
 CC platelets, including during development e.g. embryogenesis, modulating
 CC inflammation and/or thrombosis, and modulating platelet aggregation and
 CC degranulation. They are also useful for modulating disorders associated
 CC with abnormal or aberrant megakaryocyte and/or platelet proliferation,
 CC migration, morphology, differentiation and/or function, e.g. bleeding
 CC disorders such as thrombocytopenia. Other diseases which may be
 CC modulated by these antibodies are thrombotic disorders, cerebral
 CC vascular diseases (e.g. stroke and ischaemia), venous thromboembolism
 CC diseases (e.g. diseases involving leg swelling, pain and ulceration,
 CC pulmonary embolism, etc); coronary diseases (e.g. cardiovascular
 CC diseases including angina pectoris, myocardial infarction, coronary
 CC restenosis, atherosclerosis, etc); immunological disorders,
 CC developmental disorders, embryonic disorders, liver disorders, cerebral
 CC vascular diseases, venous thromboembolism disease, coronary diseases,
 CC and metastatic cancers. The antibodies of the invention only causes a
 CC transient decrease in platelet counts, platelet aggregation, and/or
 CC platelet activation and so have some advantages over prior art
 CC methods. The present sequence represents a protein sequence used to
 CC create the antibodies of the invention.
 XX

RESULT ?
 ABU11221
 ABU11221 standard; Protein: 339 AA.
 XX

3C Sequence 339 AA;

Query Match Best Local Similarity 100.0%; Score 1304; DB 24; Length 339;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQQGPGVNDLYRLEKLSSRYQDCAVIFIPAMKR 60
2: QSGPLPKPSLQALPSSLVPLEKPVTLRCQQGPGVNDLYRLEKLSSRYQDCAVIFIPAMKR 80

QY 61 SLAGRGRCSYQONGSLSWLSLPSDOLELVATGVFAKPSLSAQPGPAVSQGGDVTLCQTRYGF 120
81 SLAGRGRCSYQONGSLSWLSLPSDOLELVATGVFAKPSLSAQPGPAVSQGGDVTLCQTRYGF 140

QY 124 DQFALKYKEGDPAPYKNPERWYRASFPITIVTAHSGTYRCYSFSSRDPYLWSAPSOPLEL 180
141 DQFALKYKEGDPAPYKNPERWYRASFPITIVTAHSGTYRCYSFSSRDPYLWSAPSOPLEL 200

QY 182 VVTGTSVTPSLRPTEPSSVAEFPSEATAELTVSFTNKVFETTSRSITSPKEDSPAGP 240
201 VVTGTSVTPSLRPTEPSSVAEFPSEATAELTVSFTNKVFETTSRSITSPKEDSPAGP 260

QY 242 ARQVYTGN 249
DB 261 ARQVYTGN 269

RESULT 8

AY72791
ID AY72791 standard; Protein: 369 AA.
XX AC AY72791;
XX DT 31-MAY-2001 (first entry)
XX DE Human GPVI external domain-yeast alpha factor chimera.
XX KW Human; platelet membrane glycoprotein VI; GPVI; thrombolytic; therapy;
KW vascular disease; thrombosis; plasmid pPICZGPVI; chimeric protein.
XX OS Chimeric - Saccharomyces cerevisiae.
XX FH Chimeric - Homo sapiens.

Key Region
FT :location/Qualifiers
FT /label= Human GPVI external domain
FT /note= "Corresponds to 21-269 residues of human
GPVI protein (AY72791);"
FT 347..363
FT /label= Myc_epitope
FT 364..369
FT /label= His_tag

RESULT 9

ABP72518
ID ABP72518 standard; Protein: 501 AA.
XX AC ABP72518;
XX DT 23-MAY-2003 (first entry)
XX DE Immunoglobulin Fc-glycoprotein VI fusion protein.
XX KW Glycoprotein VI; GPVI; thrombolytic; anticoagulant; antianginal;
KW cardiovascular; Platelet; collagen; immunoglobulin; antibody;
KW human; mouse; murine; drug screening; nonadhesive; surface coating.
XX CS Chimeric - Homo sapiens.
CS Chimeric - Mus sp.
CS Synthetic.

Key Region
FT :location/Qualifiers
FT /label= Mouse_antibody_signal_peptide
FT Protein
FT /label= Mature_protein

FT Region
FT /label= Fc
FT Region
FT /label= Linker
FT Region
FT /label= Glycoprotein_VI
XX WO2003008454-A2.

CC Disclosure; Fig 5; 74pp; English.

CC The present sequence is a chimeric protein encoded by pPICZGPVI DNA. The pPICZGPVI encodes human platelet membrane glycoprotein VI (GPVI) external domain, a yeast alpha-factor, myc epitope and a histidine (His) tag. The pPICZGPVI is used to produce a soluble recombinant (sr) GPVI. The medicament comprising GPVI is useful for treating vascular disease, and for reducing platelet activation which involves contacting platelets with the medicament. The extracellular portion of GPVI is used therapeutically to attenuate platelet activation and aggregation and to treat thrombosis and other vascular diseases. Antibodies generated against GPVI are used as research and immunotherapeutic agents.

CC Sequence 369 AA;

Query Match Best Local Similarity 100.0%; Pred. No. 3.9e-105; Length 369;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQQGPGVNDLYRLEKLSSRYQDCAVIFIPAMKR 60
98 QSGPLPKPSLQALPSSLVPLEKPVTLRCQQGPGVNDLYRLEKLSSRYQDCAVIFIPAMKR 157

QY 61 SLAGRGRCSYQONGSLSWLSLPSDOLELVATGVFAKPSLSAQPGPAVSQGGDVTLCQTRYGF 120
158 SLAGRGRCSYQONGSLSWLSLPSDOLELVATGVFAKPSLSAQPGPAVSQGGDVTLCQTRYGF 217

QY 181 VVTGTSVTPSLRPTEPSSVAEFPSEATAELTVSFTNKVFETTSRSITSPKEDSPAGP 240
278 VVTGTSVTPSLRPTEPSSVAEFPSEATAELTVSFTNKVFETTSRSITSPKEDSPAGP 337

QY 241 ARQVYTGN 249
DB 339 ARQVYTGN 346

RESULT 10

ABP72518
ID ABP72518 standard; Protein: 501 AA.
XX AC ABP72518;
XX DT 23-MAY-2003 (first entry)
XX DE Immunoglobulin Fc-glycoprotein VI fusion protein.
XX KW Glycoprotein VI; GPVI; thrombolytic; anticoagulant; antianginal;
KW cardiovascular; Platelet; collagen; immunoglobulin; antibody;
KW human; mouse; murine; drug screening; nonadhesive; surface coating.
XX CS Chimeric - Homo sapiens.
CS Chimeric - Mus sp.
CS Synthetic.

Key Region
FT :location/Qualifiers
FT /label= Mouse_antibody_signal_peptide
FT Protein
FT /label= Mature_protein

FT Region
FT /label= Fc
FT Region
FT /label= Linker
FT Region
FT /label= Glycoprotein_VI
XX WO2003008454-A2.

CC Anti-thrombotic medicament, comprising a polypeptide having the extracellular domain of platelet membrane glycoprotein VI or its variant, useful for treating a vascular disease and reducing platelet activation.

XX
PC 30-JAN-2003.
XX
PR 12-JUL-2002; 2002WO-EP07796.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Burger C, Gleitz J, Frech M;
XX
DR WPI; 2003-229561/22.
XX
PT New Glycoprotein VI (GPVI) fusion protein for preventing or treating thrombotic or cardiovascular disorders, comprises a tag molecule and a non-immunoglobulin molecule, e.g. protein or oligopeptide with biological activity of GPVI.
XX
PS Claim 9; Page 19-21; 42pp; English.
CC
The present sequence is that of a fusion protein comprising an immunoglobulin Fc portion joined via a tripeptide linker to a glycoprotein VI (GPVI). The fusion protein includes a mouse antibody N-terminal signal peptide. GPVI is a major platelet glycoprotein which forms a complex with the Fc-gamma common subunit. The GPVI subunit contains a collagen binding site and the Fc-gamma subunit is responsible for signalling. The present Fc-GPVI fusion protein can be obtained by recombinant DNA methods, and is an example of fusion proteins of the invention in which GPVI is linked to a tag such as myc, GST, HA, FLAG, STREP or, preferably, the Fc portion of an immunoglobulin. Such fusion proteins can be used to screen for agonists or antagonists of GPVI-collagen and/or platelet-collagen interactions, and for the treatment of thrombotic and cardiovascular events and disorders related to GPVI-collagen and/or platelet-collagen interactions including increased platelet activation with collagen, atherosclerotic plaque rupture, unstable angina or during surgical treatment such as percutaneous transluminal coronary angioplasty (claimed). The fusion proteins are also useful for coating artificial surfaces to render them nonadhesive for cells, for modifying intraocular lenses to lessen the thrombogenicity of the lens material, for contacting the lens surface, and for covalent crosslinking to modify the lens material (all claimed).
XX
Sequence 501 AA;

Query Match 100.0%; Score 1304; DB 24; Length 501;
Best local Similarity 100.0%; Pred. No. 5.9e-105;
Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGGPGVLDYRREKLSSRYQDOAVLFIPAMKS 60
253 QSGPLPKPSLQALPSSLVLPJKEPKVTLRCQGGPGVLDYRREKLSSRYQDOAVLFIPAMKR 312
Qy 61 SLAGRGRCSYONGSLWLSLPSDQELEIATGVFAKPSLSAQPGAVSSGGDVTCQCTRYGF 120
313 SLAGRGRCSYONGSLWLSLPSDQELEIATGVFAKPSLSAQPGAVSSGGDVTCQCTRYGF 372
Db 121 DQFALYKEGDPAPYKQPERWYRASFPITVTAAHSGTYRCYSFSSRDPYWSAPSDELEZ 180
373 DQFALYKEGDPAPYKQPERWYRASFPITVTAAHSGTYRCYSFSSRDPYWSAPSDELEL 432
Qy 181 VWTGTSVTPSRLPTEPPSSVAEPESEATELTSPINKFTETRSITSPKESDSPAGP 240
433 VWTGTSVTPSRLPTEPPSSVAESEATAELTSPINKFTETRSITSPKESDSPAGP 492
Qy 241 ARQYTTKGN 249
493 ARQYTTKGN 501
DB RESULT 1C
ID ABP72519 standard; Protein; 512 AA.

XX
AC ABP72519;
XX
DT 23-MAY-2003 (first entry)
XX
DE Glycoprotein VI-immunoglobulin Fc fusion protein.
XX
KW Glycoprotein VI; GPVI; thrombolytic; anticoagulant; antianginal; cardiovascular; platelet; collagen; immunoglobulin; antibody; human; drug screening; nonadhesive; surface coating.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key location/Qualifiers
FT Peptide 1..25
FT /label= Oncostatin_M_signal_peptide
FT Protein 26..512
FT /label= Mature_protein
FT Region 26..32
FT /label= Linker
FT Region 33..281
FT /label= FC
FT Region 282..284
FT /label= Linker
FT Region 285..512
FT /label= Glycoprotein_VI
XX
PN WO2003008454-A2.
XX
PD 30-JAN-2003.
XX
PR 12-JUL-2002; 2002WO-EP07796.
XX
PA (MERE) MERCK PATENT GMBH.
XX
PI Burger C, Gleitz J, Frech M;
XX
DR WPI; 2003-229561/22.
XX
PT New Glycoprotein VI (GPVI) fusion protein for preventing or treating thrombotic or cardiovascular disorders, comprises a tag molecule and a non-immunoglobulin molecule, e.g. protein or oligopeptide with biological activity of GPVI.
XX
PS Claim 9; Page 21-23; 42pp; English.
CC
The present sequence is that of a fusion protein comprising an immunoglobulin Fc portion joined via a tripeptide linker to the Fc portion of immunoglobulin. The fusion protein includes a human oncostatin M N-terminal signal peptide. GPVI is a major platelet glycoprotein which forms a complex with the Fc-gamma common subunit. The GPVI subunit contains a collagen binding site and the Fc-gamma subunit is responsible for signalling. The present Fc-GPVI fusion protein can be obtained by recombinant DNA methods, and is an example of fusion proteins of the invention in which GPVI is linked to a tag such as myc, GST, HA, FLAG, STREP or, preferably, the Fc portion of an immunoglobulin. Such fusion proteins can be used to screen for agonists or antagonists of GPVI-collagen and/or platelet-collagen interactions, and for the treatment of thrombotic and cardiovascular events and disorders related to GPVI-collagen and/or platelet-collagen interactions including increased platelet activation with collagen, atherosclerotic plaque rupture, unstable angina or during surgical treatment such as percutaneous transluminal coronary angioplasty (claimed). The fusion proteins are also useful for coating artificial surfaces to render them nonadhesive for cells, for modifying intraocular lenses to lessen the thrombogenicity of the lens material, for contacting the lens surface, and for covalent crosslinking to modify the lens material (all claimed).
XX
Sequence 512 AA;

Query Match	Score	DB	Length	Best Local Similarity	Score	DB	Length	CC
Matches	100.0%	24	512	Local	13C4	24	512	CC
	Conservative	100.0%	0	Mismatches	0	Indels	0	Gaps
Y	1	QSGPLPKPSLQCALPSSLWPIEKFVTRCCGPPGWDYRLEKUSSRSRYQDPAVLFIPAMKR	600	Y	100.0%	Score 13C4; DB 24; Length: 512;	Y	CC
b	33	QSGPLPKPSLQALPSSLWPIEKFVTRCCGPPGWDYRLEKUSSRSRYQDPAVLFIPAMKR	922	b	100.0%	Pred. No. 6e-105;	b	CC
b	61	SIAGGRYRCSYQNGSLWSIPLSDQLEIATGVFEAKPSLSAQCPGPAAVSSGGWTLCCOTRGF	12	b	100.0%	Index 0;	b	CC
b	93	SLAGRIRCSYQNGSLWSIPLSDQLEIATGVFEAKPSLSAQCPGPAAVSSGGWTLCCOTRGF	15	b	100.0%	Gaps 0;	b	CC
b	121	DQFTLYKEGDAPYKNPERWYRASFPPEAELTVSFTNKYFTEERSRSMTT2KEDSPAGP	24	b	100.0%	Indels 0;	b	CC
b	153	DQFALYKEGDAPYKNPERWYRASFPPEAELTVSFTNKYFTEERSRSMTT2KEDSPAGP	21	b	100.0%	Score 13C4; DB 24; Length: 512;	b	CC
b	181	VVTGTSVTPSRPTEPPSSVAEFSEATAELTVSFTNKYFTEERSRSMTT2KEDSPAGP	24	b	100.0%	Score 13C4; DB 24; Length: 512;	b	CC
b	213	WTGTSVTPSRPTEPPSSVAEFSEATAELTVSFTNKYFTEERSRSMTT2KEDSPAGP	27	b	100.0%	Score 13C4; DB 24; Length: 512;	b	CC
b	241	ARQYVTKGN 249		b	100.0%	Score 13C4; DB 24; Length: 512;	b	CC
b	273	AROYYTKGN 281		b	100.0%	Score 13C4; DB 24; Length: 512;	b	CC
	RESULT 11							
X	AB61273							
X	AAB61273 standard; Protein; 339 AA.							
X	AAB61273;							
T	04-APR-2001 (first entry)							
E	Human TANGO 268-related protein #1.							
X	Human; TANGO 268; cardiact; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI; platelet membrane Glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; ischaemia; cardiovascular disease; immunological disease; liver disorder; cancer.							
X	Homo sapiens.							
S								
X	WS2C0100810-A1.							
X	WS2C0100810-A1.							
F	34-JAN-2001.							
F	30-JUN-2000; 2000WO-US18152.							
R	30-JUN-1999; 99US-0345468.							
R	06-DEC-1999; 99US-0454824.							
R	14-FEB-2000; 2000US-0503387.							
X	(MILL-) MILLENNIUM PHARM INC.							
X	Bustfield SJ, Villelal J, Jandrot-Perrus M, Vainchenker W, Gill DS; Qian MD, Kingsbury G;							
X	WPI; 2001-080877/C9.							
X	N-PSDB; AAF29484.							
X	New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders -							
X	Disclosure; Page 213-214; 227pp; English.							
PS	The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor glycoprotein VI (GPVI), also called TANGO 268. The GPVI polynucleotides							

and polypeptides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPII. These disorders include bleeding disorders (e.g. thrombocytopaenia), blood vessel injury, thrombotic disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebra, artery diseases (e.g. stroke and ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent acute cardiac ischaemia following angioplasty and metastatic cancers, especially of the colon and liver.

XX DR WPI: 2001-080877/09.
 DR N-PSDB; AAF29485.

XX PT New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders.

XX PS Disclosure; Page 214-215; 227pp; English.

CC The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent, cure cardiac ischaemia following angioplasty and metastatic cancers, especially of the colon and liver.

XX SQ Sequence 339 AA:

Query Match 99.7%; Score 1300; DB 22; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.8e-105; Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGGPLPKPSIQLAPSSIVPLEKPVTLRCQGPGVLDYRLEKSSSRYQDOAVLFIPAMKR 60
 21 QSGGPLPKPSIQLAPSSIVPLEKPVTLRCQGPGVLDYRLEKSSSRYQDOAVLFIPAMKR 80

Db 61 SLAGRYRCSYONGSILWSPSDQELVATGVFAKPLSQAQGPAGVSSGGDVTIQCQTRYGF 120
 81 SLAGRYRCSYONGSILWSPSDQELVATGVFAKPLSQAQGPAGVSSGGDVTIQCQTRYGF 140

QY 121 DQFALYKEGDPAPYKPERWYRASPIITVTAHSGTYRCYSFSSRDPYLNSAPSDPLEL 180
 141 DQFALYKEGDPAPYKPERWYRASPIITVTAHSGTYRCYSFSSRDPYLNSAPSDPLEL 200

QY 181 VVTGTSVTPSLRPTEPSSVAEFESEATAELTVSFINKVFTTETRSRSTSITSPKESDSPAGP 240
 201 VVTGTSVTPSLRPTEPSSVAEFESEATAELTVSFINKVFTTETRSRSTSITSPKESDSPAGP 260

Db 241 ARQYYTKGN 249

Cb 261 ARQYYTKGN 269

RESULT 13

ID AAB61275 standard; Protein; 339 AA.

XX AC AAB61275;

XX DT 04-APR-2001 (first entry)

DE Human TANGO 268-related protein #3.

KW Human; TANGO 268; cardiot; cerebroprotective; cytostatic; anticoagulant; thrombolytic; antiarteriosclerotic; haemostatic; glycoprotein VI; GPVI; platelet membrane glycoprotein receptor; bleeding disorder; blood vessel injury; thrombotic disorder; haemorrhagic disorder; stroke; ischaemia; cardiovascular disease; immunological disease; liver disorder; cancer.

XX OS Homo sapiens.

PN WO200100810-A1.

XX PD 04-JAN-2001.

XX PR 30-JUN-2000; 2000WO-US18152.

XX PR 30-JUN-1999; 99US-0345468.

PR 06-DEC-1999; 99US-0454624.

PR 14-FEB-2000; 2000US-0503387.

XX PR (MIU-) MILLENNIUM PHARM INC.

XX PI Busfield SC, Villella J, Jandrot-Perrus M, Vainchenker W, Gill DS; Qian MD, Kingsbury G;

DR WPI: 2001-080877/09.

DR N-PSDB; AAF29486.

XX PT New genes encoding human platelet-expressed collagen receptor, glycoprotein VI, and its modulators, useful for preventing, treating and diagnosing hemorrhagic disorders, thrombotic diseases and immunological disorders.

XX PS Disclosure; Page 216; 227pp; English.

CC The present sequence is given in a specification relating to an isolated nucleic acid molecule encoding a platelet membrane glycoprotein receptor (GPVI), also called TANGO 268. The GPVI polynucleotides and polypeptides and their modulators, e.g. antisense nucleic acids, ribozymes and antibodies, are useful for preventing, treating and diagnosing disorders associated with aberrant expression or activity of GPVI. These disorders include bleeding disorders (e.g. thrombocytopenia), blood vessel injury, thrombotic disorders (e.g. thrombotic occlusion of the coronary arteries), haemorrhagic disorders, coronary artery and cerebral artery diseases (e.g. stroke and ischaemia), cardiovascular diseases (e.g. atherosclerosis and myocardial infarction), immunological diseases (e.g. platelet disorder) and embryonic liver disorders. Preferably they are used to prevent, cure cardiac ischaemia following angioplasty and metastatic cancers, especially of the colon and liver.

XX SQ Sequence 339 AA:

Query Match 99.7%; Score 1300; DB 22; Length 339;
 Best Local Similarity 99.6%; Pred. No. 7.8e-105; Matches 248; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGGPLPKPSIQLAPSSIVPLEKPVTLRCQGPGVLDYRLEKSSSRYQDOAVLFIPAMKR 60
 21 QSGGPLPKPSIQLAPSSIVPLEKPVTLRCQGPGVLDYRLEKSSSRYQDOAVLFIPAMKR 80

Db 61 SLAGRYRCSYONGSILWSPSDQELVATGVFAKPLSQAQGPAGVSSGGDVTIQCQTRYGF 120
 81 SLAGRYRCSYONGSILWSPSDQELVATGVFAKPLSQAQGPAGVSSGGDVTIQCQTRYGF 140

QY 121 DQFALYKEGDPAPYKPERWYRASPIITVTAHSGTYRCYSFSSRDPYLNSAPSDPLEL 180
 141 DQFALYKEGDPAPYKPERWYRASPIITVTAHSGTYRCYSFSSRDPYLNSAPSDPLEL 200

QY 181 VVTGTSVTPSLRPTEPSSVAEFESEATAELTVSFINKVFTTETRSRSTSITSPKESDSPAGP 240
 201 VVTGTSVTPSLRPTEPSSVAEFESEATAELTVSFINKVFTTETRSRSTSITSPKESDSPAGP 260

Db 241 ARQYYTKGN 249

Cb 261 ARQYYTKGN 269

RESULT 14

ID AAB61276

XX AC AAB61276;

CC diseases (e.g. diseases involving leg swelling, pain and ulceration, pulmonary embolism, etc); coronary diseases (e.g. cardiovascular diseases including angina pectoris, myocardial infarction, coronary restenosis, atherosclerosis, etc); immunological disorders, developmental disorders, embryonic disorders, liver disorders, cerebral vascular diseases, venous thromboembolism disease, coronary diseases, and metastatic cancers. The antibodies of the invention only causes a transient decrease in platelet counts, platelet aggregation, and/or platelet activation and so have some advantages over prior art methods. The present sequence represents a protein sequence used to create the antibodies of the invention.

xx

Sequence 339 AA;

Query Match: 99.7%; Score 1300; DB 24; Length 339;
 Best Local Similarity 99.6%; Pct. No. 7.8e-05; Mismatches 1; Indels 0; Gaps 0;
 Matches 248; Conservative 0; N mismatches 1;

QY	1	QSGPLPKPSLQALPSSVPELEKPVILRCQSPGVQJYREKISSSRYQCAVLEIPAVKR	60
Db	21	QSGPLPKPSLQVLPSJVPELEKPVILRCQQGPFGVDIYRLEKISSSRYQDAVJFIPAVKR	80
QY	61	SIAGRVRCSYONGSIVSWSLPSDCELEVATGVFAKPSLSAQPGPAVSSGGDTQGCTRYGF	120
Db	81	SLAGRYRCSYONGSIVSWSLPSDCELEVATGVFAKPSLSAQPGPAVSSGGDTQGCTRYGF	140
QY	121	DQFALYKEGDAPYCNPERWYRASFPITVTAHSGTYRCYSFSSRDPYLWSAASDPL	180
Db	141	DQFALYKEGDAPYCNPERWYRASFPITVTAHSGTYRCYSFSSRDPYLWSAASDPL	200
QY	181	VWTGTSVTPSLPTEPPSSVAEFSERATELLTIVSFINKVFTETRSRISITSPKESSESPAGP	240
Db	201	VWTGTSVTPSLPTEPPSSVAEFSERATELLTIVSFINKVFTETRSRISITSPKESSESPAGP	260
QY	241	ARQYTKGN 249	
Db	261	ARQYTKGN 269	

Search completed: November 10, 2003, 06:16:57
 Job time : 43 secs

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OM protein - protein search, using sw model

Run on: November 10, 2003, 06:14:09 ; Search time 17 Seconds

688.803 million cell updates/sec
(without alignments)

Title: US-09-503-387-9
Perfect score: 1304
Sequence: 1 QSGELRKPSIQLPSSIVPL..... SPKESDSEAGRQVYTKGN 249

Scoring table: BJOSTM62
Gapcf 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026735 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 6
Maximum DB seq length: 200000000

Post-processing: Minimum Match C%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB	IP	Description
1	333	25.5	387	1	K3SI_HUMAN
2	322	24.7	304	1	K2S1_HUMAN
3	320.5	24.6	444	1	K3SI_HUMAN
4	315	24.2	304	1	K2S1_HUMAN
5	314	24.1	304	1	K2S4_HUMAN
6	314	24.1	348	1	K2L1_HUMAN
7	314	24.1	348	1	K2L2_HUMAN
8	312.5	24.0	341	1	K2L3_HUMAN
9	306.5	23.5	304	1	K2S5_MOUSE
10	302	23.2	335	1	G49B_MOUSE
11	299	22.9	287	1	FCAR_HUMAN
12	299	22.9	377	1	K2L4_HUMAN
13	297.5	22.8	304	1	K2S3_HUMAN
14	294.5	22.6	455	1	K3S2_HUMAN
15	280	21.5	303	1	G49A_MOUSE
16	143.5	11.0	495	1	A15G_HUMAN
17	136	10.4	291	1	DM43_DIDMR
18	126.5	9.7	3707	1	PGEM_MOUSE
19	123.5	9.5	267	1	FCG3_RAT
20	113.5	8.7	1284	1	NRCA_CHICK
21	111.5	8.6	4391	1	PGBM_HUMAN
22	108	8.3	341	1	FCG2_CAVPO
23	107	8.2	261	1	FCG3_MOUSE
24	106	8.1	285	1	FCG2_RAT
25	105.5	8.1	330	1	FCG2_MOUSE
26	101	7.7	1709	1	SN_HUMAN
27	101	7.7	3375	1	UN52_CAEEL
28	100	7.7	257	1	FCEA_HUMAN
29	100	7.7	1367	1	AMYH YEAST
30	99.5	7.6	727	1	PEC1_MOUSE
31	99	7.6	739	1	VCA1_HUMAN
32	98.5	7.6	3149	1	TEGU2_BBV
33	97.5	7.5	296	1	FCG2_BOVIN

KW	Repeat; Multigene family; Polymorphism.	RX	MEDLINE=95232526; PubMed=7716543;
FT	SIGNAL; 21; By SIMILARITY.	RA	Colonna M.; Samaridis J.;
FT	CHAIN; 22; 387 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR	RT	"Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B recognition by human natural killer cells.";
FT	DOMAIN; 22; 340 3DS1.	R:	Science 268:405-408 (1995).
FT	TRANSMEM; 341; 360 EXTRACELLULAR (POTENTIAL).	R:	[3]
FT	DOMAIN; 361; 387 CYTOPLASMIC (POTENTIAL).	R:	Science FROM N.A.
FT	DOMAIN; 42; 402 IG-LIKE C2-TYPE 1.	RC	TISSUE=Lymphoid;
FT	DISULFID; 137; 202 IG-LIKE C2-TYPE 2.	RX	MEUDINE=96195217; PubMed=8627176;
FT	CARBHYD; 237; 350 IG-LIKE C2-TYPE 3.	RA	Biassoni R.; Cantoni C.; Falco M.; Verdiani S.; Bottino C.; Vitale M.,
FT	CARBHYD; 49; 95 BY SIMILARITY.	RA	Conte R.; Poggi A.; Moretta A.; Moretta L.
FT	DISULFID; 144; 195 BY SIMILARITY.	RT	"The human leukocyte antigen (HLA)-C-specific 'activatory' or 'inhibitory' natural killer cell receptors display highly homologous extracellular domains but differ in their transmembrane and intracytoplasmic portions."
FT	VARIANT; 244; 293 N-LINKED (GLCNAC. . .) (POTENTIAL).	R:	J. Exp. Med. 183:645-650 (1996);
FT	CARBHYD; 179; 279 N-LINKED (GLCNAC. . .) (POTENTIAL).	R:	E. EXP. Med. 183:645-650 (1996);
FT	CARBHYD; 273; 273 N-LINKED (GLCNAC. . .) (POTENTIAL).	CC	FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES
FT	VARIANT; 166; 166 R -> H /FTID=VAR_310377.	CC	DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
SQ	SEQUENCE 387 AA; 42902 MW; 0B75CE753D15E100 CRC64;	CC	-- SUBCELLULAR LOCATION: TYPE I membrane protein.
Query Match 25.5%; Score 333; DB 1; Length 387;			
Best Local Similarity 37.3%; Pred. No. 5.2e-19; Mismatches 91; Indels 34; Gaps 7; Matches 90; Conservative 26; Mismatches 91; Indels 34; Gaps 7;			
Qy	7 KPSLQLAPSSLVPLEKPVTLRCQGPPGVLDLYRKLEK---LSSRYQQD----AVLF 55	CC	-- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
Db	123 KSSLAAHPGPVLVKSERVILQQLQSDIMFEHFLHKEWIKPSRLVGQIHGDGVSKANFSI 182	CC	-- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
Qy	56 PAMKRSLAGRYRC-----SYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSSGG 108	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and/or commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
Db	183 GSMMRALLAGTYRCYGSVTHTPYQ---LSAPSPLDIVTGYEKPSLSAQPGPKVQAGE 239	CC	CC
Qy	109 DVTLOQCOTRYGFDFALYKEGRDAPRYKGP-----ERWYRASFPITIVTAHSGTYRCYSF 163	CC	CC
Db	239 SVTLSCSSRSSYDMYHLSREGGAHERRLPAVRKVNRTFQADFL--GPATHEGTYRCFGS 296	CC	CC
Qy	164 SSR2PYWSAPSDDPLELWVTTGTSVTPSRRLPTEPSSVAESE---ATAEJCVSTNKV 219	DR	DR
Db	297 FRHSPYEWSDPSDPLLVSUTGNFSSSSWPSPEPSSKSGNLRLHILIGTSVVK--PFTLL 356	DR	EMBL; X89893; CAA61983.1; -.
Qy	219 F 219	DR	HSSP; P43626; INKR.
Db	357 F 357	DR	Genew; HGNC:6334; KIR2DS2.
RESULT 2			
K2S2_HUMAN	STANDARD; FRT; 304 AA.	DR	MIM; 604953; -.
:D	K2S2_HUMAN STANDARD; FRT; 304 AA.	DR	EMBL; X89893; CAA61983.1; -.
:C	P43631; Q14955; (Rev. 32, Created)	DR	DR
:D	01-NOV-1995 (Rev. 32, Last sequence update)	DR	GO; GO:0004882; F:transmembrane receptor activity; NAS.
:D	16-OCT-2003 (Rev. 40, Last annotation update)	DR	GO; GO:0006955; P:immune response; NAS.
:D	15-SEP-2003 (Rev. 42, Last annotation update)	DR	InterPro; IPR03599; Ig.
:D	Killer cell immunoglobulin-like receptor (KIR) class I (KIR-5)	DR	InterPro; IPR03306; Ig_MHC.
:D	NK cell receptor (Natural killer associated transcript 5) (NKAT-5)	DR	PFam; PF00047; ig; 2.
:D	(ps8 natural killer cell receptor clone CJ-49; (ps8 NK receptor) (NK receptor CJ-83 ACT).	DR	SMART; SM00409; Ig; 1.
:D	KIR2DS2 OR NKAT5.	DR	PROSITE; PS50835; Ig_LIKE; FALSE_NEG.
:D	Homo sapiens (Human).	DR	KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane; Repeat; Multigene family.
:O	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo. OX NCBI_TaxID=9606;	DR	KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane; Repeat; Multigene family.
:R	;1;	FT	BY SIMILARITY.
:R	SEQUENCE OF 2-304 FROM N.A.	FT	KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
:R	TISSUE=Natural killer cells; MEDLINE=95269128; PubMed=7749980; Wagtmann N.; Biassoni R.; Cantoni C.; Verdiani S.; Mainardi M.S., Vitale M.; Bottino C.; Moretta L.; Moretta A.; Long E.O.; "Molecular clones of the ps8 NK cell receptor reveal immunoglobulin-related molecules with diversity in both the extra- and intracellular domains"; J. Immunol. 159:439-449 (1995).	FT	2DS2.
:R	Immunity 2:439-449 (1995).	FT	EXTRACELLULAR (POTENTIAL).
:R	{2}	FT	CYTOSOLIC (POTENTIAL).
:R	SEQUENCE FROM N.A.	FT	IG-LIKE C2-TYPE 1.
Query Match 24.7%; Score 322; DB 1; Length 304;			
Best Local Similarity 33.6%; Pred. No. 2.8e-18; Mismatches 94; Indels 58; Gaps 10; Matches 93; Conservative 32; Mismatches 94; Indels 58; Gaps 10;			
Qy	7 KPSLQLAPSSLVPLEKPVTLRCQGPPGVLDLYRKLEK---LSSRYQQD----QAVI 53	CC	CC
Db	28 KPSLAAHPGPVLKSEETVILQQLQSDIVTGYEKPSLSAQPGPTVLA 85	CC	CC
Qy	54 FIPAMKRSLAGRYRC-----SYQNGSLWLSLPSDQLELVATGVFAKPSLSAQPGPAVSS 106	CC	CC
Db	86 SIGPMMQDLAGTYRCYGSVTHSPTYQ---LSAPSPLDIVTGYEKPSLSAQPGPTVLA 241	CC	CC

CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-BW4
 CC ALLELE. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
 CC CELL LYSIS.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

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 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation.
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
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 or send an email to license@isb-sib.ch).

RESULT 3

K311_HUMAN STANDARD; PRT; 444 AA.

AC P43629; C43473; Q16541;

DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Killer cell immunoglobulin-like receptor 3DII precursor (MHC class I NK cell receptor; (Natural killer associated transcript 3); (NKAT-3); (p70 natural killer cell receptor clones Ci-2/CL-1); (HLA-BW4 specific DE inhibitory NK cell receptor)).

DE KIR3DL1 OR NKAT3 OR NK31.

OS Homo sapiens (Human)

CC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CX NCBi_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Natural killer cells;

RX MEDLINE=95256; PubMed=7716543;

RA Cloringo M.; Samardzic J.;
 RT "Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B recognition by human natural killer cells.";
 RT Science 268:405-408 (1995).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood lymphocytes;

RX MEDLINE=96111957; PubMed=8777725;

RA Wagtmann N.; Rajagopalan S.; Winter C.C.; Peruzzi M.; Jong E.C.;
 RT "Killer cell inhibitory receptors specific for HLA-A and HLA-B identified by direct binding and by functional transfer.";
 RT Immunity 3:801-809 (1995).

RN [3]

RP SEQUENCE FROM N.A.

RC TISSUE=Peripheral blood lymphocytes;

RX MEDLINE=96343861; PubMed=8760804;

RA Pende D.; Biassoni R.; Cantoni C.; Verdiani S.; Falco M.;
 RA di Donato C.; Accame L.; Bottino C.; Moretta A.; Moretta L.;
 RT "The natural killer cell receptor specific for HLA-A allootypes: a novel member of the p58/p70 family of inhibitory receptors that is characterized by three immunoglobulin-like domains and is expressed as a 140-kD disulphide-linked dimer.";
 RT J. Exp. Med. 184:505-518 (1996).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Blood;

RX MEDLINE=95378652; PubMed=7650366;

RA D'Andrea A.; Chang C.; Franz-Bacon K.; McClanahan T.; Phillips J.R.;
 RA Lanier L.L.;
 RT "Molecular cloning of NKB1. A natural killer cell receptor for HLA-B allotypes.";
 RT J. Immunol. 155:2336-2340 (1995).

RN [5]

RP SEQUENCE FROM N.A., AND VARIANTs.

RX MEDLINE=9809084; PubMed=9430221;

RA Chrberk M.; Vallante N.M.; Shum B.P.; Snilling R.G.; Corliss B.; Tyan D.; Lanier L.L.; Parham P.;
 RT "Human diversity in killer cell inhibitory receptor genes.";
 RL "Community 7:753-763 (1997)."

CC

DR EMBL; J41269; AAA69870.1; -.

DR EMBL; U30273; AAB52521.1; -.

DR EMBL; J30274; AAB52522.1; -.

DR EMBL; X94262; CAA63938.1; -.

DR EMBL; U31416; AAC23725.1; -.

DR EMBL; AF022049; AAB95322.1; -.

DR PRR; G01925; G01925.

DR HSSP; P43626; INKR.

DR Genew; HGNC:6338; KIR3DL1.

DR MIM; 604946; -.

DR GO:0035887; C:integral to plasma membrane; NAS.

DR GO:0003793; F:defense/immunity protein activity; NAS.

DR GO:0030199; F:HLA-B specific inhibitory MHC class I recep. . .; NAS.

DR GO:0036955; P:immune response; NAS.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003006; Ig_YHC.

DR Pfam; PF0047; ig; 3.

DR SMART; SM00409; Ig; 3.

DR PROSITE; PSSC835; Ig_LIKE; FALSE_NEG.

DR Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane; KW Repeat; Multigene family; Polymorphism.

FT SIGNAL 1 21

FT CHAIN 22 444

FT BY SIMILARITY.

FT KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR

FT DOMAIN 22 340

FT EXTRACELLULAR (POTENTIAL).

FT DOMAIN 341 360

FT POTENTIAL.

FT TRANSMEM 361 444

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 42 102

FT IG-LIKE C2-TYPE 1.

FT DOMAIN 137 202

FT IG-LIKE C2-TYPE 2.

FT DOMAIN 237 300

FT IG-LIKE C2-TYPE 3.

FT DISULFID 49 95

FT BY SIMILARITY.

FT 144 195

FT BY SIMILARITY.

FT 244 293

FT CARBOHYD 92 179

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 179 273

FT S-->L.

FT VARIANT 2 2

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 13 13

FT L-->F.

FT /FTid=VAR_010320.

FT M-->V.

FT /FTid=VAR_010321.

FT I-->V.

FT /FTid=VAR_010322.

FT VARIANT 75 75

FT I-->L.

FT /FTid=VAR_010323.

FT G-->R.

FT /FTid=VAR_010336.

FT VARIANT 68 68

FT S-->C.

FT /FTid=VAR_010324.

FT SEQUENCE 444 AA; 49098 MW; 47DEA12BAFDEC53 CRC64;

SQ

Query Match: 24.6%; Score 320.5; DB: -, length: 444;
 Best Local Similarity: 38.6%; Pctd. No. 5.9e-18;
 Matches: 83; Conservative: 22; Mismatches: 81; Index: 29; Gaps: 5;

QY 7 KPSLQALPSSLVPEKPVTLRCQGPGVDDYRLEKLSSRYQQAV-----LFI 55

DR SMART; SM00409; IG; 1.

DR PROSITE; PS50835; IG-LIKE; FALSE-NEG.

KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;

KW Repeat; Multigene family; Polymorphism.

QY BY SIMILARITY.

DB 183 KPSILAHPGPLVKSGERVILQCLWSQDINFEHFLREGISKDPSPRLVGGIHDGVSKANFSI 182

FT SIGNAL 1 21

FT CHAIN 22 304

FT DOMAIN 22 245

FT TRANSMEM 246 264

FT DOMAIN 265 304

FT DOMAIN 42 107

FT DOMAIN 142 205

FT DISJULFD 49 100

FT DISJULFD 149 198

FT CARBOHYD 67 67

FT CARBOHYD 84 84

FT CARBOHYD 144 144

FT CARBOHYD 178 178

FT VARIANT 91 91

FT /FTid=VAR_010318.

FT SEQUENCE 304 AA; 33646 SW; 4193A542151CAE06 CRC64;

Query Match 24 2%; Score 315; DB 1; Length 304;

Best Local Similarity 34 6%; Pred. No. ie-17;

Matches 84; Conservative 31; Mismatches 90; Indels 38; Gaps 7;

Db SEQUENCE FROM N.A.

RC TISSUE=Lymphoid;

RX MEDLINE=96195217; PubMed=8627176;

RA Biassoni R., Cantoni C., Falco M., Verdiani S., Bottiro C., Vitale M.,

RA Conte R., Roggi A., Moretta A., Moretta L.;

RT 'Human leukocyte antigen (HLA)-C-specific 'activatory' or

RT 'inhibitory' natural killer cell receptors display highly homologous

RT extracellular domains but differ in their transmembrane and

RT intracytoplasmic portions.';

J. Exp. Med. 183:645-650(1996).

[2]

RF SEQUENCE FROM N.A. AND VARIANT LYS-91.

RX MEDLINE=98090086; PubMed=943C221;

RA Uhrlberg M., Vaiante N.M., Shum B.P., Shilling H.G.,

RA Lienert-Weidenbach K., Corliss B., Tyan J., Larier J.L., Parham P.;

RT "Human diversity in killer cell inhibitory receptor genes.";

RL Immunity 7:753-763(1997);

CC --!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.

CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.

CC SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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--

CC EMBL; XAA9892; CAA61982; 1;

CC DR EMBL; AF022046; AAB95319; 1; -.

DR HSSP; P43626; INKR.

DR GeneW; HGNC:6333; KIR2DS1.

DR MM; 604952; -.

DR GO:0016021; C:integral to membrane; NAS.

DR GO; GO:0004888; F:transmembrane receptor activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR033599; IG.

DR InterPro; IPR003006; IG_MRC.

DR Pfam; PF00047; Ig; 2.

RESULT 4

K2S1_HUMAN STANDARD; PRT; 304 AA.

QY 014954; O43471; 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, last annotation update)

DE Killer cell immunoglobulin-like receptor 2DS1 precursor (MHC class II NK cell receptor Bb Act).

GN KIR2DS1.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Lymphoid;

RX MEDLINE=96195217; PubMed=8627176;

RA Biassoni R., Cantoni C., Falco M., Verdiani S., Bottiro C., Vitale M.,

RA Conte R., Roggi A., Moretta A., Moretta L.;

RT 'Human leukocyte antigen (HLA)-C-specific 'activatory' or

RT 'inhibitory' natural killer cell receptors display highly homologous

RT extracellular domains but differ in their transmembrane and

RT intracytoplasmic portions.';

J. Exp. Med. 183:645-650(1996).

[2]

RF SEQUENCE FROM N.A. AND VARIANT LYS-91.

RX MEDLINE=98090086; PubMed=943C221;

RA Uhrlberg M., Vaiante N.M., Shum B.P., Shilling H.G.,

RA Lienert-Weidenbach K., Corliss B., Tyan J., Larier J.L., Parham P.;

RT "Human diversity in killer cell inhibitory receptor genes.";

RL Immunity 7:753-763(1997);

CC --!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.

CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.

CC SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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--

CC EMBL; XAA9892; CAA61982; 1;

CC DR EMBL; AF022046; AAB95319; 1; -.

DR HSSP; P43626; INKR.

DR GeneW; HGNC:6333; KIR2DS1.

DR MM; 604952; -.

DR GO:0016021; C:integral to membrane; NAS.

DR GO; GO:0004888; F:transmembrane receptor activity; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR033599; IG.

DR InterPro; IPR003006; IG_MRC.

DR Pfam; PF00047; Ig; 2.

RESULT 5

K2S4_HUMAN STANDARD; PRT; 304 AA.

QY 014952; 01-NOV-1995 (Rel. 32, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE K2S4 immunoglobulin-like receptor 2DS4 precursor (MHC class I NK cell receptor) (Natural killer cell receptor associated transcript 8' (NKAT-8) (P58 natural killer cell receptor clone C5-39) (P58 NK receptor) (CL-17).

DE KIR2DS4 OR NKAT8 CR KKA3.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Natural killer cells;

RX MEDLINE=95269128; PubMed=7749980;

RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainati M.S., Vitale M., Bottino C., Moretta A., Long E.O.;

RT Molecular clones of the p58 NK cell receptor reveal immunoglobulin-related molecules with diversity in both the extra- and intracellular domains.;"

RT Immunity 2:439-449(1995).

RL Immunity 2:439-449(1995).

RN [2] ·
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9627004; PubMed=8662091;
 RA Boehring C., Samaridis J., Colonna M.;
 RT "Alternatively spliced forms of human killer inhibitory receptors.";
 RL Immunogenetics 44:227-230(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lymphoid;
 RX MEDLINE=9635C503; PubMed=8765026;
 RA Bottino C., Sivori S., Vitale M., Cantoni C., Falco M., Perdew D.,
 Morelli L., Augugliaro R., Semenzato G., Biassoni R., Moretta L.,
 RA Moretta A.;
 RT "A novel surface molecule homologous to the p58/p50 family of
 receptors is selectively expressed on a subset of human natural
 killer cells and induces both triggering of cell functions and
 proliferation.";
 RL Eur. J. Immunol. 26:1816-1824(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Char H.W., Salter R.J.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.
 CC -- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
 CC -- DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC -- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
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 CC
 DR EMBL: U24077; AAC50336.1; ALT_NIT.
 DR EMBL: L76671; AA336599.1; -.
 DR EMBL: X94609; CAA64317.1; -.
 CR EMBL: AF002255; AAB61281.1; -.
 DR HSSP; P43626; INKR.
 DR Genew; HGNC:6336; KIR2DS4.
 DR MIM; 604955; -.
 DR GO; GO:0005897; C:integral to plasma membrane; TAS.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR0033006; Ig_MHC.
 DR Pfam; PF00407; Ig_1.
 DR SMART; SMC0409; Ig_1.
 DR PROSITE; PS50835; Ig_LIKE; FALSE_NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 304 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 246 265 POTENTIAL.
 FT DOMAIN 266 304 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 107 Ig-LIKE C2-TYPE 1.
 FT DOMAIN 142 205 Ig-LIKE C2-TYPE 2.
 FT DISULFID 149 100 BY SIMILARITY.
 FT DISULFID 149 198 BY SIMILARITY.
 FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 304 AA; 33583 MN; CEFDAFF3FD679AJF CRC64;

Query Match: 24.1%; Score 314; DB 1; Length 304;
 Best Local Similarity 36.3%; Fred. No. 1.2e-17;
 Matches 90; Conservative 3C; Mismatches 92; Indels 36; Gaps 9;

QY : QSGPLPKPSLQALPSSLVPLEKPTILRCQGPPGV---LYRJEKLSSRY----QC 49
 Db 22 QEGVHRKRSFLALPQGHLVKSEETVILQCWSDVMFHFLHLREGKENNLHLHGEHDGV 81
 QY 50 QAVLFIPAMKRSUAGRYRC----SYQNGSLWLSLPDOLELEVATGVFAKPSISAOPGP 102
 Db 82 KANFSIGPMMPVLAGTGYCGSVPHSPYQ---LSAAPSPLDMVIGLYEKPSLSAQPGP 137
 QY 103 AVSSGGEVTLCQTRYGFQDFAYKEGDPAPYKNP----ERWYRASPIITVTAAGST 157
 Db 138 TVQAGENTVLSCSSRSSYDMYHLSREGEAHERRIAPAVRSINGFQADFPL--GPATHGTT 195
 QY 158 YRCYSFSSRQ-PYLWSAPSAPSDPYLELWVGTTSVTPSRLPTEPPSSVAEFESE----ATAELT 211
 Db 196 YRCFG-SFRDAPYEWNSNSDPLLVSVTGNPNSNWPSPTEPSSKGPNRHLHVLLGTSWK 254
 QY 212 VSFTNKVF 219
 Db 255 IPFTILLF 262

RESULT 6
 K2L1_HUMAN STANDARD; PRT: 348 AA.
 ID P43626; O4347C;
 AC C1-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 2B1 precursor (MHC class I
 DE NK cell receptor) (Natural killer associated transcript 1) (NKAT-1)
 DE (p58 natural killer cell receptor ciones CL-42/A7.11) (p58 NK
 DE receptor) (p58.1 MHC class-I specific NK receptor).
 GN KIR2DL1 OR NKAT1 OR CL158A.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC NCBIXPAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Natural killer cells;
 RX MEDLINE=95232526; PubMed=7716543;
 RA Colonna M., Samaridis J., Moretta L., Moretta A., Long S.O.;
 RA "Cloning of immunoglobulin-superfamily members associated with HLA-C
 and HLA-B recognition by human natural killer cells.";
 RT Science 268:405-408(1995).
 RN [2]
 RP SEQUENCE FROM N.A. AND SEQUENCE OF 22-45.
 RC TISSUE=Natural killer cells;
 RX MEDLINE=95269128; PubMed=7716540;
 RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainardi M.S.,
 RA Vitale M., Bottino C., Moretta L., Moretta A., Long S.O.;
 RA "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-
 related molecules with diversity in both the extra- and intracellular
 domains.";
 RT Immunity 2:439-449(1995).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANTS.
 RX MEDLINE=98090086; PubMed=9430221;
 RA Uhrberg M., Valiante N.M., Shurn B.P., Shilling H.G.,
 RA Corliss B., Tyan D., Lanier L.L., Parham P.;
 RA "Human diversity in killer cell inhibitory receptor genes.";
 RT Immunity 7:753-763(1997).
 RL [4]
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 27-221.
 RX MEDLINE=9743335; PubMed=9288975;
 RA Fan Q.R., Mosyak L., Winter C.C., Wagtmann N., Long E.O., Wiley D.C.;
 RT "Structure of the inhibitory receptor for human natural killer cells
 resembles haematopoietic receptors.";
 RT Nature 389:96-100(1997).
 CC INHIBITS THE ACTIVITY OF NK CELLS THIS PREVENTING CELL LYSIS.
 CC -- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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CC

DR EMBL; U4267; AAA69868.1; -.

DR EMBL; U24376; AAC50335.1; -.

DR EMBL; U24378; AAC50337.1; -.

DR PIR; A56247; A56247.

DR PDB; INKR; 11-NOV-98.

DR PDB; 1IM9; 30-MAY-01.

DR Genew; HGNC; 6329; KIR2D1L.

DR MIN; 604936; -.

DR GO; GO:0005887; C:integral tc plasma membrane; TAS.

DR GO; GO:0004872; F:receptor activity; TAS.

DR GO; GO:0006955; F:immune response; TAS.

DR Interpro; IPR003599; Ig.

DR Interpro; IPR003006; Ig_MHC.

DR P5am; PF00047; ig; 2.

DR SMART; SM00409; PROSITE; PS50835; Ig_LIKE; FALSE NEG.

KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;

KW Repeat; Multigene family; Polymorphism; 3D-structure.

FT SIGNAL 1 21 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR

FT CHAIN 22 348 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 22 245 POTENTIAL.

FT TRANSMEM 246 264 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 265 348 IG-LIKE C2-TYPE 1.

FT DOMAIN 42 107 IG-LIKE C2-TYPE 2.

FT DISULFID 142 205

FT DISULFID 149 198 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARIANT 5 5 V->F.

FT VARIANT 37 37 /FTId=VAR_003950.

FT VARIANT 135 135 P->L.

FT VARIANT 175 175 /FTId=VAR_003951.

FT VARIANT 184 184 P->T.

FT VARIANT 203 203 D->N.

FT VARIANT 237 237 H->R.

FT VARIANT 266 266 /FTId=VAR_010333.

FT VARIANT 266 266 K->E.

FT STRAND 32 34 R->C.

FT STRAND 38 40 /FTId=VAR_010335.

FT STRAND 41 42

FT STRAND 45 51

FT STRAND 57 63

FT STRAND 68 73

FT STRAND 75 77

FT TURN 78 79

FT STRAND 80 87

FT HELIX 92 94

FT STRAND 96 104

FT TURN 105 106

FT STRAND 107 107

PT TURN 108 109

Query Match 24.1%; Score 314; DB 1; Length 348;

Best Local Similarity 32.3%; Pred. No. 1.4e-17; Gaps 10;

Matches 93; Conservative 36; Mismatches 105; Index 54; Gaps 10;

Matches 93; Conservative 36; Mismatches 105; Index 54; Gaps 10;

Qy 7 KPSLQAIAPSSLVPLEKPVTLRCCQGPPGVBLVRLEKLSSRYQD-----CAVL 53

Db 28 KPSLLAHGPPIJKSBEETVILQCKNSDMFEHFLHR--EGMFNDTIRLIGEHHDGVSKANP 85

Qy 54 FIPAMKRSLAGRYRC-----SYONGSLMSPSDQLELVATGVFAKPSISACPGPAVSS 106

Db 86 SISRMTQDLAGTYRCYGSVTHSPYQ---VSAPSQPLDIVIGLYEKPSLSAQPGPTVLA 141

Qy 107 GGDVTIQCQTRYGFDPALYKEGDPAPYKNP----ERWYRASFPITVTAHSGYRCY 161

Db 142 GENVTLSCSSRSSYDWHISREGEAHERRLPAGPKVNGTFOADEPL-GPATGGTYRCF 199

Qy 162 SFSSRDPYLMSAPSDDPLELWVTTGTSTVTPSLRPTEPSSVA----EFSEATAELTVSF-- 214

Db 200 GSFHDSPPYSWSKSSDPLIVSVGNPNSNSWPSPTEPSSKTGNPRHLHILIGTSVIIIFL 259

Qy 215 -----TNK---VFTETTSRITSPKESDSPAGPARQYTKGN 249

Db 260 LFFJLHRWCSNKXNAVMDQESAGNRTANSESDDE-QDQEVTYQIN 306

RESJST 7

IC K2L2_HUMAN

AC P43627; Q14951; STANDARD; PRT; 348 AA.

DT 01-NOV-1995 (Rel. 32, Created)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Killer cell immunoglobulin-like receptor 2D₂ precursor (MHC class I killer cell receptor) (Natural killer cell receptor clone CL-43) (p58 NK receptor).

DE (p58 natural killer cell receptor clone CL-43) (p58 NK receptor).

DE KIR2D12 OR NK46.

CS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Actinopterygii; Sarcopterygii; Teleostei; Euteleostomi; CX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Natural killer cells;

RX MEDLINE=95269128; PubMed=7749980;

RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Mainiati M.S.,

RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.C.;

RA "Molecular clones of the p58 NK cell receptor reveal immunoglobulin-related molecules with diversity in both the extra- and intracellular domains." J. Immunol. 159: 151-156 (1997).

RA R1 [2]

RA SEQUENCE FROM N.A.

RX MEDLINE=96273004; PubMed=8662091;

RA Dohring C., Samardis J., Colonna M.;

RA "Alternatively spliced forms of human killer inhibitory receptors." Immunogenetics 44:227-230 (1996).

CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C
 CC ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
 CC CELM LYSIS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
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 or send an email to license@isb-sib.ch').

CC DR InterPro; IPR033599; Ig; 1.
 CC DR InterPro; IPR033006; Ig_MHC.
 CC DR Pfam; PF0047; Ig; 2.
 CC DR SMART; SM00409; Ig; 1.
 CC DR PROSITE; PS50935; Ig_LIKE; FALSE_NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family; 3D-structure;
 FT SIGNAL 1 2; BY SIMILARITY.
 FT CHAIN 22 348 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 2212.
 FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 246 264 POTENTIAL.
 FT DOMAIN 265 348 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 107 Ig-LIKE C2-TYPE 1.
 FT DOMAIN 142 205 Ig-LIKE C2-TYPE 2.
 FT DISULFIC 49 1C0 BY SIMILARITY.
 FT DISULFID 149 198 BY SIMILARITY.
 FT CARBOHYC 84 34 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYC 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYC 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 289 293 SE -> RQ (IN REF. 2).
 SQ 348 AA; 39472 MW; 5B54C548F5CF3FB CRC64;

Query Match 24.1%; Score 314; DB 1; length: 348;
 Best Local Similarity 32.4%; Pred. No. 1.4e-17; Indels 58; Gaps 11;
 Matches 94; Conservative 36; Wismatches 102; Index 58; Gaps 11;

OY 7 KPSIQLALPSSLVPLEKPVTLRQQGPPGVPIYRLEKLSSSRYYQD-----QAVL 53
 Db 28 KPSLAAHPGRIVKSEETVILQGWSDVRFERFELHR-EGFKKDTHLIGERHHGDGVSKANF 85

QY 54 FIPAMKRSLAGRYRC-----SYONGSLNSLPSDLQELVATGVFKAPKSLAQGPVSS 106
 Db 86 SIGPMMODLAGTYRCYGSVTSPYQ---LSAPSDPLDIVITGLYEKPKSLAQGPVTA 140

QY 1C7 GGDVTLQOCTRYGFQFALKYKED-----PAPYKPNPERWYRASPFIITVTAHSGTYR 159
 Db 142 GESVTLSRSSRSDYMHLSREGEAHECRFSAGPKVNGT--FQADPPL-GPATGGTYR 197

QY 160 CYSFSSRDPYIWSAPSDEPLEWVIGTSVTPSLPTEPPSSVA---EFSEATEELGVSF 214
 Db 198 CFGSFRDSPYEWNSNNSDPLVSVIGNPSNSWPSPTEPSSKTNPRHJHILGTSWVILP 257

QY 215 -----TNK---VFTTETRSITSPKESDPSAGPARQYTKGN 249
 Db 258 ILRFLFLHRWCNSNKNAAVMDGESAGNRTANSEDSDE-QDPQEVTYQLN 306

RESULT 8
 ID K2L3_HUMAN STANDARD; PRT; 341 AA.

AC P43628; 043472;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Killer cell immunoglobulin-like receptor 2D13 precursor (MHC class I NK cell receptor) (Natural killer associated transcript 2; (NKAT-2; (p58 natural killer cell receptor clone CL-6); (p58 NK receptor) (p58.2 MHC class-I specific NK receptor)).
 DE GN KIR2D13 OR NKAT2 OR CD158B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homioidea; Homo; NCBI_TAXID=9606; [1].
 RN RP SEQUENCE FROM N.A.
 RC TISSUE=Natural killer cells;
 RX MEDLINE=95232526; PubMed=7716543;
 RA Colonna M., Samardis J.;
 RT "Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B recognition by human natural killer cells.";
 RL Science 268:405-408(1995).
 RN RP SEQUENCE FROM N.A.
 RP TISSUE=Natural killer cells;
 RX MEDLINE=95269128; PubMed=7749980;
 RA Wagtmann N., Biassoni R., Cantoni C., Verdiani S., Malattia M.S.,
 RA Vitale M., Bottino C., Moretta L., Moretta A., Long E.O.;
 RT "Volatile clones of the p58 NK cell receptor reveal immunoglobulin-related molecules with diversity in both the extra- and intracellular domains.";
 RT Immunity 2:439-449(1995).
 [3]
 RN RP SEQUENCE FROM N.A., AND VARIANTS ALA-9; ARG-32; GLU-56; ARG-71 AND HIS-318.
 RP MEDLINE=98C090086; PubMed=9430221;
 RX Unbergen M., Valiante N.M., Shum B.P., Shilling H.G.,
 RA Liener-Weidenbach K., Corliss B., Tyar D., Lanier L.L., Farham P.;
 RT "Human diversity in killer cell inhibitory receptor genes.";
 RL Immunity 7:753-763(1997).
 CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
 CC -!- INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
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CC DR InterPro; IPR033006; Ig_MHC.
 CC DR Pfam; PF0047; Ig; 2.
 CC DR SMART; SM00409; Ig; 1.
 CC DR PROSITE; PS50835; Ig_LIKE; FALSE_NEG.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family; Polymorphism.
 FT SIGNAL 1 21 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT CHAIN 22 341 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 FT 2D13.

PT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
 PT TRANSMEM 246 265 POTENTIAL; CYTOPLASMIC (POTENTIAL).
 PT DOMAIN 266 341 CYTOPLASMIC (POTENTIAL).
 PT DOMAIN 42 107 Ig-like C2-type 1;
 PT DISULFID 142 205 Ig-like C2-type 2.
 PT DISULFID 49 103 BY SIMILARITY.
 PT CARBOHYD 149 198 BY SIMILARITY.
 PT CARBOHYC 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT VARIANT 9 9 /FTid=VAR_G10313.
 PT VARIANT 32 32 /FTid=VAR_G10314.
 PT VARIANT 56 56 Q->E.
 PT VARIANT 71 71 E->R.
 PT SEQUENCE 318 318 /FTid=VAR_G10316.
 Query Match 24.0%; Score 312.5; DB 1; Length 341;
 Best Local Similarity 37.4%; Pred. No. 1.8e-17;
 Matches 82; Conservative 24; Mismatches 76; Indels 37; Gaps 7;
 PT SEQUENCE 341 AA; 37886 MW; C21EAFF80EA9AAB2 CRC64;
 PT SIGNAL 7 KFLSQLQALPSSLVPLKEKPVTLRQQGPGVLDLYREKLSSSRYYQD----QAVL 53
 Db 28 KPSLLAHPGPLVKSEETVILQWSDVRQFHFLHR--EGKFKDTLHLIGEHGVSXANF 85
 Qy 54 FIPAMKRSLAGRYRC-----SYQNGSLWLSPLSDQLELVATGVFAKPSLSAQPGPAVSS 106
 Db 86 SIGPMMODLAGTYRCYGSVTHSPVQ---LSAPSTCPDLDIVITGLYEKPSLSAQPGPTVLA 141
 Qy 1C7 GGDVTLQOCQTRYGFQFALKYKEGD-----PAPYKNPERWYRASPIIITVAHSGTYR 159
 Db 142 GESVTISSLSSRSSYDMHISREGEEAHERRFSAGPKVNGT--FQAFPL--GPATGGTYR 197
 Qy 16C CYSFSSRDPYWLWAPSAPSDPLEVLVNTGTSVTPSLRPTEPS 198
 Db 198 CGFSFRDSDPYEWNSNDDPLLVSVTGPNNSNWPSPTEFSS 236
 RESULT 9
 K2S5_HUMAN STANDARD; PRT; 304 AA.
 AC Q14953;
 DT 01-NOV-1997 (Rel. 35, Created;
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Killer receptor; immunoglobulin-like receptor 2ES5 precursor (NK Class I NK cell receptor); (Natural killer associated transcript 9; NK2.2).
 GN KIR2DS5 OR NKAT3.
 CS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OX NCBI_TaxID=9606;
 RN [1] SEQUENCE FROM N.A. MEDLINE=9627004; PubMed=8662391;
 RA Doehring C., Samaridis J., Colonna M.;
 RT "Alternatively spliced forms of human killer inhibitory receptors.";
 RL Immunogenetics 44:227-230(1996).
 CC -!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
 CC DCES NOT INHIBIT THE ACTIVITY OF NK CELLS.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
 CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
 CC
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 CC
 CC
 DR EMBL; L76672; AAB36600.1; -.
 DR HSSP; P43626; 1NKR.
 DR Genew; HGNC:6337; KIR2D55.
 DR MIM; 604956; -.
 GO; GO:0005887; C: integral to plasma membrane; NAS.
 DR GO; GO:0030110; F: HLA-C specific inhibitory MHC class I recep. . .; NAS.
 CR InterPro; IPR033599; Ig.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00409; Ig; 1.
 DR PROSITE; PS50835; Ig-LIKE; PMS_E_NEG.
 DR Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 KW Repeat; Multigene family.
 PT SIGNAL 1 21 BY SIMILARITY.
 PT CHAIN 22 304 BY SIMILARITY.
 PT TRANSMEM 22 245 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
 PT DOMAIN 265 304 2DS5.
 PT DOMAIN 42 107 EXTRACELLULAR (POTENTIAL).
 PT DOMAIN 142 205 CYTOPLASMIC (POTENTIAL).
 PT DISULFID 49 100 Ig-like C2-type 2.
 PT DISULFID 149 198 BY SIMILARITY.
 PT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT CARBOHYD 223 223 N-LINKED (GLCNAC. . .) (POTENTIAL).
 PT SEQUENCE 304 AA; 33644 MW; F0BD73BFA3DE35DB CRC64;
 Query Match 23.5%; Score 306.5; DB 1; Length 304;
 Best Local Similarity 36.3%; Pred. No. 4.6e-17;
 Matches 78; Conservative 26; Mismatches 82; Indels 29; Gaps 5;
 PT SEQUENCE 7 KPSLLAHPGPLVKSEETVILQWSDVRQFDLHREGENTHTLRLIGEHIDGVSKGNFSI 87
 Qy 28 KPSLLAHPGPLVKSEETVILQWSDVRQFDLHREGENTHTLRLIGEHIDGVSKGNFSI 87
 RESULT 10
 G49B_MOUSE STANDARD; PRT; 335 AA.
 AC Q49B_MOUSE 064281; O64312;
 DT 01-NOV-1997 (Rel. 35, Created;
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Mast cell surface glycoprotein GP49B precursor.
 GN GP49B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurograthi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1] SEQUENCE FROM N.A. (ISOFORMS GP49B1 AND GP49B2).
 RP STRAIN=C3H, and BALB/C; TISSUE=Bone marrow;
 RC MEDLINE=94:79223; PubMed=8132564;
 RA Castells M.C., Wu X., Arm J.P., Austen K.F., Katz H.R.;

Urberg M., Valiante N.M., Shum B.P., Shilling H.G., Liemert-Weidenbach K., Corliss B., Tyan D., Lanier L.L., Parham P.; RA "Human diversity in killer cell inhibitory receptor genes."; RT Immunity 7:753-763(1997). [5]

SEQUENCE FROM N.A. (ISOFORM 2).

RA Chan H.W., Saiter R.D.; RT "Exon deletion contributes to structural diversity of 2D4 killer inhibitory receptors.;" Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases. [6]

SEQUENCE FROM N.A. (ISOFORM 2).

RX MEDLINE=97213129; Pubmed=9059894;

RA Selvakumar A.; PT "Polymorphism and domain variability of human killer cell inhibitory receptors.;" RL Immunol. Rev. 155:183-196 (1997); Event=Alternative splicing; Named isoforms=6;

CC Name=1; IsoId=Q99736-1; Sequence=Displayed;

CC Name=2; Synonyms=AST; IsoId=Q99706-3; Sequence=VSP_002609;

CC Name=4; Synonyms=ASD1; IsoId=Q99706-4; Sequence=VSP_002609, VSP_002610; Name=5; Synonyms=ASD2; IsoId=Q99706-5; Sequence=VSP_002609, VSP_002610, VSP_002610; Name=6; IsoId=C99706-6; Sequence=VSP_002608, VSP_002609, VSP_002610; -! SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

-! SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.

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CC DR EMBL; U71199; AAB49756.1; -. DR EMBL; AF0303123; AAB61926.1; -. DR EMBL; AF003116; AAB61926.1; JOINED. DR EMBL; AF003117; AAB61926.1; JOINED. DR EMBL; AF003118; AAB61926.1; JOINED. DR EMBL; AF003119; AAB61926.1; JOINED. DR EMBL; AF003121; AAB61926.1; JOINED. DR EMBL; AF003122; AAB61926.1; JOINED. DR EMBL; AF003120; AAB61926.1; JOINED. DR EMBL; AF002979; AAB71387.1; -. DR EMBL; AF002980; AAB71388.1; -. DR EMBL; AF002981; AAB71389.1; -. DR EMBL; AF002982; AAB71390.1; -. DR EMBL; X97229; CAA65868.1; -. DR EMBL; X99479; CAA67842.1; -. DR EXBL; X99480; CAA67843.1; -. DR EMBL; X99481; CAA67844.1; -. DR EMBL; AF034771; AAB95164.1; -. DR EMBL; AF034772; AAB95165.1; -. DR EMBL; AF010035; AAD24763.1; -. DR EMBL; AF110032; AAD24763.1; JOINED. DR EMBL; AF110033; AAD24763.1; JOINED. DR EMBL; AF110034; AAD24763.1; JOINED. DR EMBL; U73394; AAC51146.1; -. DR Genew; HGNC:6332; KIR2DL4. DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0004888; F:transmembrane receptor activity; TAS. DR GO; GO:0006968; P:cellular defense response; TAS. DR GO; GO:0037165; P:signal transduction; TAS.

DR InterPro; IPR003006; Ig_MHC.

DR PROSITE; PSS0835; Ig_LIKE; FALSE_NEG.

KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane; Repeat; Multigene family; Alternative splicing; Polymorphism.

RN CHAIN SIGNAL 1 21 BY SIMILARITY.

RN DOMAIN TRANSMEM 22 242 BY SIMILARITY.

RN DOMAIN 243 263 BY SIMILARITY.

RN DOMAIN 264 377 BY SIMILARITY.

RN DOMAIN 44 104 BY SIMILARITY.

RN DOMAIN 139 202 BY SIMILARITY.

RN DISULFID 51 97 BY SIMILARITY.

RN DISULFID 146 195 BY SIMILARITY.

RN CARBOHYD 141 141 BY SIMILARITY.

RN CARBOHYD 175 175 BY SIMILARITY.

RN VARSPLIC 27 121 BY SIMILARITY.

FT TRANSMEM 22 242 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 243 263 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 264 377 IG-LIKE C2-TYPE 1.

FT DOMAIN 44 104 IG-LIKE C2-TYPE 2.

FT DISULFID 51 97 BY SIMILARITY.

FT DISULFID 146 195 BY SIMILARITY.

FT CARBOHYD 141 141 BY SIMILARITY.

FT CARBOHYD 175 175 BY SIMILARITY.

FT VARSPLIC 27 121 BY SIMILARITY.

FT VARSPLIC 219 235 /FTId=VSP_002608.

FT VARSPLIC 219 235 Missing (in isoform 2, isoform 4, isoform 5 and isoform 6).

FT VARSPLIC 219 235 /FTId=VSP_002609.

FT VARSPLIC 219 235 Missing (in isoform 3, isoform 4, isoform 5 and isoform 6).

FT VARSPLIC 219 235 /FTId=VSP_002610.

FT VARSPLIC 219 235 Missing (in isoform 5).

FT VARSPLIC 219 235 /FTId=VSP_002611.

FT VARIANT 53 53 Y->C.

FT VARIANT 87 87 /FTId=VAR_010307.

FT VARIANT 87 87 ;->V.

FT VARIANT 87 87 /FTId=VAR_010308.

FT VARIANT 138 138 T->A.

FT VARIANT 138 138 /FTId=VAR_010309.

FT VARIANT 209 209 A->P.

FT VARIANT 209 209 /FTId=VAR_010310.

FT VARIANT 271 271 D->N.

FT VARIANT 371 371 /FTId=VAR_010311.

FT VARIANT 371 371 H->N.

FT CONFLICT 229 229 /FTId=VAR_010312.

FT CONFLICT 377 AA; 41527 MW; T->P (IN REF 5).

FT SEQUENCE 377 AA; 41527 MW; 7ECAECFOCF4143B CRC64;

Query Match 22.9%; Score 239; DB 1; Length 377;

Best Local Similarity 34.2%; Pred. No. 2. 3e-16;

Matches 78; Conservative 36; Mismatches 94; Indexes 20; Gaps 1;

Qy 3 GPLRKPSIQLPSSVPLEKPTLRGGPPGVLYREKLUSS-----SRYQDQAVLF1 55

Db 26 GGQDKPFCSAWPSAVVPOGGHVLRLCHYRGRGNFIIFTLYKKDGVPVPELYNRIFWNFSFIS 83

Qy 56 PAMKRSLAGRYRC---SYQNGSLWLSPSDQCLMIVATGVFAKPSLSACGPGPAVSS3GDVTL 11

Db 86 P-LTPAHAGTYRCRGFPHSPTEWSAPSAPSNPLVIMVTGLYKEPKSILTARPGPVTIGENVIL 14

Qy 113 QCQTRYGFDFALYKEGDPAPYKNP----EWYRASFPTITVTAHSGYTCYCSFSSRD 16

Db 145 SCSSQSSFDIYLSREGAEHLRPAVPSINGTFOADFPL-GPATGETYRCFGSFPHGS 20

Qy 168 PYLWSAPSAPDPLELUVVTGTSTPSRLPTEP--PSAWAFSEATAELTVS 213

Db 203 PYEWSDAASDPLPVSVGNPSSSWPSPTPEKTIQIARHLHAVRYSVA 25C

RESULT 13

K2S3_HUMAN ID_K2S3_HUMAN STANDARD; PRT; 304 AA.

AC Q14952; O03644; 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT C1-NOV-1997 (Rel. 42, Last annotation update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Killer cell immunoglobulin-like receptor 2DS3 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 7) (NKAT-7).
DE KIR2DS3 OR NKAT7.
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9627004; PubMed=8662091;
RA Doehring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RL ImmunoGenetics 44:227-230(1996).
RN [2]
RP SEQUENCE FROM N.A.
RA Biassoni R.;
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
CC -!!- FUNCTION: RECEPTOR CN NATURAL KILLER (NK) CELLS FOR HLA-C ALLELES.
CC DOES NOT INHIBIT THE ACTIVITY OF NK CELLS.
CC -!!- SUBCELLULAR LOCATION: TYPE I membrane protein.
CC -!!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR K352_HUMAN
DR K352_HUMAN STANDARD; PRIM; 455 AA.
AC P43630; Q13238; Q14947; Q14946; Q92684; Q95367;
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Killer cell immunoglobulin-like receptor 3DL2 precursor (MHC class I
DE NK cell receptor) (Natural killer associated transcript 4) (NKAT-4)
DE (p70 natural killer cell receptor cinc CL-5).
GN KIR3DL2 OR NKAT4.
DS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Natural killer cells;
RX MEDLINE=9523256; PubMed=7716543;
RA Colonna M., Samaridis J.;
RT "Cloning of immunoglobulin-superfamily members associated with HLA-C
and HLA-B recognition by human natural killer cells.";
RT Science 268:405-408(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood lymphocytes;
RX MEDLINE=96111977; PubMed=8777725;
RA Wagtmann N, Rajagopalan S, Winter C.C., Peruzzi M, Long E.C.,
RT "Killer cell inhibitory receptors specific for HLA-C and HLA-B
identified by direct binding and by functional transfer.";
RT immunity 3:801-809(1995).
RN [3]
RP SEQUENCE FROM N.A., AND VARIANT VAL-113.
RC TISSUE=Lymphoid;
RX MEDLINE=96343861; PubMed=8760804;
RA Pende D., Biassoni R., Bottino C., Verdiani S., Falco M.,
Ra di Donato C., Accame L., Bottino C., Moretta A., Moretta L.;
RT "The natural killer cell receptor specific for HLA-A allotypes: a
novel member of the p58/p70 family of inhibitory receptors that is
characterized by three immunoglobulin-like domains and is expressed as
RT a 140-kD disulphide-linked dimer.";
RT J. Exp. Med. 184:505-518(1996).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=9527004; PubMed=8662091;
RA Doehring C., Samaridis J., Colonna M.;
RT "Alternatively spliced forms of human killer inhibitory receptors.";
RT Immunogenetics 44:227-230(1996).
RN [5]
RP VARIANTS ALA-40; VAL-113; ASP-158; HIS-166; PRO-223 AND THR-252.
RX MEDLINE=98090086; PubMed=9430221;
RA Uhrberg M., Valiante N.M., Shum B.P., Shilling H.G.,
RA Lienert-Weidenbach K., Corliss B., Yan D., Lanier L.L., Parham P.,
RT "Human diversity in killer cell inhibitory receptor genes.";
RT immunity 7:753-763(1997).
RN -!!- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-A ALLELES.
RN INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING CELL LYSIS.
CC -!!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
CC -!!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
QY 107 GGDVTLCQTRYGFQFALYKEGD-----PAPYKPERWYASPFPIITVAAHSGYR 159
QY 142 GESVTLSCSSSSYYDMHISTEGEAHERRFSAGPKVNGT--FOADFLP-GPATGGTYR 197
Db 160 CYSFSSRDPYLMSAPSDE:WVYTGTSVTPSLRPTEP 199
Db 198 CFGSPHDSPYEWNSKSDPLLVSVTGNPSNWSPSPEPP 236

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CC EMBL; L41270; AAA69871.1; -.

CC EMBL; U30272; AAB52520.1; -.

CC EMBL; X93595; CAA63791.1; -.

CC EMBL; X94373; CAA64150.1; -.

CC EMBL; L76665; AAB36593.1; -.

CC EMBL; L76666; AAB36594.1; -.

DR HSSP; P43626; INR.

DR Genew; HGNC; 6339; KIR3DL2.

DR MIM; 604947; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0003822; F:MHC-interacting protein; TAS.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig_3.

DR SMART; SM00409; Ig_2.

DR PROSITE; PS50835; Ig_LIKE; FALSE_NEG.

KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;

KW Repeat; Multigene family; Polymorphism.

FT SIGNAL 1 21 BY SIMILARITY.

FT CHAIN 22 455 KILLER CELL IMMUNOGLOBULIN-LIKE RECEPTOR
3C2L.

FT DOMAIN 22 340 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 341 360 POTENTIAL.

FT DOMAIN 361 455 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 42 102 Ig-LIKE C2-TYPE 1.

FT DOMAIN 137 262 Ig-LIKE C2-TYPE 2.

FT DOMAIN 237 300 Ig-LIKE C2-TYPE 3.

FT DISULFID 49 95 BY SIMILARITY.

FT DISULFID 144 195 BY SIMILARITY.

FT CARBOHYD 244 293 BY SIMILARITY.

FT CARBOHYD 179 179 N-LINKED (GAGNAc. . .) (POTENTIAL).

FT CARBOHYD 239 239 N-LINKED (GAGNAc. . .) (POTENTIAL).

FT CARBOHYD 273 273 N-LINKED (GAGNAc. . .) (POTENTIAL).

FT CARBOHYD 306 306 N-LINKED (GAGNAc. . .) (POTENTIAL).

FT VARIANT 40 40 P -> A. /FTId=VAR_010325.

FT VARIANT 113 1:3 L -> V. /FTId=VAR_010326.

FT VARIANT 158 158 E -> D. /FTId=VAR_010327.

FT VARIANT 166 166 R -> H. /FTId=VAR_010328.

FT VARIANT 228 228 A -> P. /FTId=VAR_010329.

FT VARIANT 252 252 L -> T. /FTId=VAR_010330.

FT SEQUENCE 455 AA; 5C230 MW; D343A6BB6B3C2945 CRC64;

Query Match 22.6%; Score 294.5; DB 1; Length 455;

Best Local Similarity 32.6%; Pred. No. 6.6e-16;

Matches 89; Conservative 35; Mismatches 104; Indels 45; Gaps 10;

Matches 89; Conservative 35; Mismatches 104; Indels 45; Gaps 10;

QY 3 GPLPKPSQLPSSIVPLEKPVTRRCQQPPGVDIRLEKJSSSR-----YQDQAVL- 53

QY 24 GGQDKPELSARPSTVPRGGHVALLQCHYRRGENEMLYKEKDRTSHVPIFHGRIFQESFIMG 83

QY 54 -FIPAMKRSLAGRYRCSYQNGS-----WSLPSDQELEVATGVFAKPSLSAQCPGPVASS 106

QY 84 PVTPAH---AGTYRC--RGSRPHSLTGWSAPSNSPLVIMVTGNHRKPSLLAHPGPLIKS 136

QY 107 GGEVTLQCCQTRYGFQDPAKYKEDPAPYKPERWY-----RASFPILTVAHSGY 158

QY 137 GETVILQCCWSDVMFEEFFHREGIS--EDPSRLVGQZHGVSKANFSIGPLMPVLGTY 193

QY 159 RCYSFSSRDPYLWSAPSDPPLMVTGTSVTSPSRPTEPSSVAESEATAELTVSFTNKV 216

Db	194 RCGSVPHSPYQLSAPSDPLDVITGLYEKPS-LSAQGP3P7VQAGENVTLSRSSWSSYD:	252
Qy	219 FITET----SRSITTSFK-----ESDSPAGPA 241	
Db	253 YHLSREGEAHEERRLRAVPKVNRRTFQADFPLGPA 285	
Cy	1 QSGPLPKPSLQLALPSSLVPLEKPVTLRCQGPPGVDLYRLEKLUSSSRVQDDAV-----52	
Db	22 QAGHLRKPKIWAEPGSVIAATSVIWCWSWEAQYYVLDKEKSWNPDTEVPLRNKT 81	
Cy	53 -LFIPAMKRSLAGFVRCSYQNGSLWLSLPSDQE-LATGVFAKPSLSAQPGPANVSSGGDVT 111	
RESULT 15		
G49A_MOUSE		
ID_G49A_MOUSE	STANDARD;	PRT; 303 AA.
AC_061450;		
DT_01-NOV-1997	(Rel. 35, Created)	
DT_15-SEP-2003	(Rel. 42, last annotation update)	
DE_Mast cell surface glycoprotein GP49A precursor.		
GN_GP49A OR GP49.		
OS_Mus musculus (Mouse).		
OC_Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OC_NCBI_TAXID=10090;		
OX_OX		
RP_SEQUENCE FROM N.A., AND SEQUENCE OF 24-45.		
RC_STRAIN=BALB/C; TISSUE=Bone marrow;		
RX_MEDLINE=91340742; Pubmed=714901;		
RA_Arm J.P., Gurish M.F., Reynolds D.S., Scott H.C., Gartner C.S.,		
RA_Austen K.F., Katz H.R.,		
RT_Molecular cloning of gp49, a cell-surface antigen that is preferentially expressed by mouse mast cell progenitors and is a new member of the immunoglobulin superfamily.;		
RL_J. Biol. Chem. 266:15966-15973(1991).		
CC_-- FUNCTION: MAY PLAY A ROLE IN CELL-CELL OR CELL-CYTOKINE		
CC_INTERACTIONS DURING THE DEVELOPMENT OF MAST CELLS.		
CC_-- SUBCELLULAR LOCATION: Type I membrane protein.		
CC_-- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.		
CC		
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CC		
CC_EMBL; M65C27; AAA37479.1; -.		
DR		
KSSP; P43626; INKR.		
DR		
MGD; MG:102702; Gp49a.		
DR		
InterPro; IPR007110; Ig-like.		
DR		
PROSITE; PS50835; IG_LIKE_1.		
KW_Signal; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat.		
FT_SIGNAL_1_23	MAST CELL SURFACE GLYCOPROTEIN GP49A.	
FT_CHAIN_24_303	EXTRACELLULAR (POTENTIAL).	
FT_DOMAIN_24_238	POTENTIAL.	
FT_TRANSMEM_239_260	CYTOSOLIC (POTENTIAL).	
FT_DOMAIN_261_303	IG-LIKE C2-TYPE 1.	
FT_DOMAIN_42_125	IG-LIKE C2-TYPE 2.	
FT_DISULFID_124_212	POTENTIAL.	
FT_DISULFID_49_98	POTENTIAL.	
FT_DISULFID_144_196	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT_DISULFID_79_99	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT_CARBOHYD_133_133	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT_CARBOHYD_191_191	N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQSEQUENCE_303_AA_34194 MW; D165659BFAB9C40D CRC64;		
Query Match 21.5%; Score 280; DB 1; Length 303;		
Best Local Similarity 32.1%; Pred. No. 5.5e-15;		
Matches 75; Conservative 35; Mismatches 96; Indels 28; Gaps 5;		

Db 92 KPKIRFMATASYAGIVNYKSAAGPSEHSDAMELVMGAYENPSLSVYFSSNNTSGVIS 141
Qy 112 LQCOTRYGFDOFFALYKEGDPAVPKNPERW-----YRASFPITVTAAHSGYRC 160
Dx 142 FKCSSSTLFGRFLIQEG---KGHLSTMDSQHCANQPTHATFVFLDAVAPNHNGTFRC 196
Qy 161 YSFSSRRDPYJWSAPSOPLELVVGTSVTRSLRPTEPSSVAESEAELTVSF 214
Db 197 YGFFRNEPQWSKPSNSIDLMISETK-EQSCTPTE--DGJETYQKLIGVLWSE 247

Search completed: November 10, 2003, 06:16:04
Job time : 19 secs

Best Local Similarity 100.0%; **Pred.** No. 2.3e-11; **Matches** 249; **Conservative** 0; **Mismatches** 0; **Indels** 0; **Gaps** 0;

Query : QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVLYRLEKLUSSRYQDAVLFIPAMKR 60

DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVLYRLEKLUSSRYQDAVLFIPAMKR 80

Query 61 SLAGRYRCSYONGSLWSLPSQDQEELVATGVFAKPSLSAQPGRPAVSSGGDVTLCQTRYGF 120

DB 81 SLAGRYRCSYONGSLWSLPSQDQEELVATGVFAKPSLSAQPGRPAVSSGGDVTLCQTRYGF 140

Query 121 DQFALYKEGPAPYKPNPERWYRASFPILTVAHSCTYRCYSFSSRDPYLWSAPSDELE 180

DB 141 DQFALYKEGPAPYKPNPERWYRASFPILTVAHSCTYRCYSFSSRDPYLWSAPSDELE 200

Query 181 VVTGTSVTPSLPTEPPSSVAESEATAELTUSFTNKVFETTSRSITSPKESDSPAGP 240

DB 201 VVTGTSVTPSLPTEPPSSVAESEATAELTUSFTNKVFETTSRSITSPKESDSPAGP 260

Query 241 ARQYYTKGN 249

DB 261 ARQYYTKGN 269

RESULT 2

ID Q9HCN6 **PRELIMINARY;** **PRT;** 620 AA.

AC Q9HCN6; **DT** 01-MAR-2001 (**TREMBrel.** 16, **Created**)

DT 01-MAR-2001 (**TREMBrel.** 16, **Last sequence update**)

DT 01-MAR-2003 (**TREMBrel.** 23, **Last annotation update**)

DE Platelet glycoprotein VI-2.

GN GPVI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN NCBI_TaxID=9606;

RX MEDLINE=20483673; PubMed=11027634;

RA Ezumi Y., Uchiyama T., Takayama H.; "Molecular cloning, genomic structure, chromosomal localization, and alternative splice forms of the platelet collagen receptor glycoprotein VI"; Biochem. Biophys. Res. Commun. 277:27-36(2000).

DR EMBL; AB043820; BAB12246.1; -.

DR DR HSSP; P43626; INR.

DR InterPro; IPR03599; IgI.

DR InterPro; IPR033006; Ig_MHC.

DR Pfam; PF00497; Ig; 2.

DR SMART; SM00409; Ig; 2.

SQ SEQUENCE 321 AA; 35158 NM; 93FBF88945958345 CRC64;

Query Match Best Local Similarity 91.6%; Score 1194; DB 4; Length 321; **Matches** 231; **Conservative** 0; **Mismatches** 0; **Indels** 18; **Gaps** 1;

Query : QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVLYRLEKLUSSRYQDAVLFIPAMKR 60

DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVLYRLEKLUSSRYQDAVLFIPAMKR 80

Query 62 SLAGRYRCSYONGSLWSLPSQDQEELVATGVFAKPSLSAQPGRPAVSSGGDVTLCQTRYGF 120

DB 82 SLAGRYRCSYONGSLWSLPSQDQEELVATGVFAKPSLSAQPGRPAVSSGGDVTLCQTRYGF 140

Query 123 DQFALYKEGPAPYKPNPERWYRASFPILTVAHSCTYRCYSFSSRDPYLWSAPSDELE 180

DB 142 DQFALYKEGPAPYKPNPERWYRASFPILTVAHSCTYRCYSFSSRDPYLWSAPSDELE 200

Query 183 VVTGTSVTPSLPTEPPSSVAESEATAELTUSFTNKVFETTSRSITSPKESDSPAGP 240

DB 203 VVTGTSVTPSLPTEPPSSVAESEATAELTUSFTNKVFETTSRSITSPKESDSPAGP 260

Query 242 ARQYYTKGN 249

DB 243 ARQYYTKGN 251

RESULT 3

ID Q9HCN7 **PRELIMINARY;** **PRT;** 321 AA.

AC Q9HCN7; **DT** 01-MAR-2001 (**TREMBrel.** 16, **Created**)

DT 01-MAR-2001 (**TREMBrel.** 16, **Last sequence update**)

DT 01-MAR-2003 (**TREMBrel.** 23, **Last annotation update**)

DE Platelet glycoprotein VI-2.

GN GPVI.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN RN RPI [?]

RX SEQUENCE FROM N.A.

RA Ezumi Y., Uchiyama T., Takayama H.; "Molecular cloning, genomic structure, chromosomal localization, and alternative splice forms of the platelet collagen receptor glycoprotein VI"; Biochem. Biophys. Res. Commun. 277:27-36(2000).

DR DR EMBL; AB043820; BAB12246.1; -.

DR DR HSSP; P43626; INR.

DR InterPro; IPR03599; IgI.

DR InterPro; IPR033006; Ig_MHC.

DR Pfam; PF00497; Ig; 2.

DR SMART; SM00409; Ig; 2.

SQ SEQUENCE 321 AA; 35158 NM; 93FBF88945958345 CRC64;

Query Match Best Local Similarity 92.8%; Score 1194; DB 4; Length 321; **Matches** 231; **Conservative** 0; **Mismatches** 0; **Indels** 18; **Gaps** 1;

Query : QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVLYRLEKLUSSRYQDAVLFIPAMKR 60

DB 21 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPPGVLYRLEKLUSSRYQDAVLFIPAMKR 80

Query 63 SLAGRYRCSYONGSLWSLPSQDQEELVATGVFAKPSLSAQPGRPAVSSGGDVTLCQTRYGF 120

DB 83 SLAGRYRCSYONGSLWSLPSQDQEELVATGVFAKPSLSAQPGRPAVSSGGDVTLCQTRYGF 140

Query 124 DQFALYKEGPAPYKPNPERWYRASFPILTVAHSCTYRCYSFSSRDPYLWSAPSDELE 180

DB 143 DQFALYKEGPAPYKPNPERWYRASFPILTVAHSCTYRCYSFSSRDPYLWSAPSDELE 200

Query 184 VVTGTSVTPSLPTEPPSSVAESEATAELTUSFTNKVFETTSRSITSPKESDSPAGP 240

DB 204 VVTGTSVTPSLPTEPPSSVAESEATAELTUSFTNKVFETTSRSITSPKESDSPAGP 260

Query 244 ARQYYTKGN 249

DB 245 ARQYYTKGN 251

RESULT 4

ID Q8MJZ2 **PRELIMINARY;** **PRT;** 481 AA.

AC Q8MJZ2; **DT** 01-OCT-2002 (**TREMBrel.** 22, **Created**)

DT 01-OCT-2002 (**TREMBrel.** 22, **Last sequence update**)

DT 01-MAR-2003 (**TREMBrel.** 23, **Last annotation update**)

DE Leukocyte immunoglobulin-like receptor.

GN LIRE.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

RN RN RPI [?]

RX SEQUENCE FROM N.A.

RA MEDLINE=2155186; PubMed=11698452;

DB Canavez F.C., Young N.T., Guethlein L.A., Rajalingam R., Khakoo S.I..

RA Shum B.P.; Parham P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 reveals framework and rapidly evolving genes.";
 RI J. Immunol. 167:5786-5794(2001).
 DR EMBL; AF383169; AAL31878.1; -.
 DR InterPro; IPR03598; Ig_C2.
 DR InterPro; IPR00306; Ig_MHC.
 DR Pfam; PF00047; ig; 4.
 DR SMART; SM00408; IGC2; 4.
 KW Immunoglobulin domain; Receptor.
 SQ SEQUENCE 481 AA; IGC2; 4.
 32.6%; Score 424.5; DB 6; Length: 481;
 Best Local Similarity 42.3%; Pred. No. 1.7e-30;
 Matches 91; Conservative 34; Mismatches 69; Indels 21; Gaps 3;
 Query Match 32.6%; Score 424.5; DB 6; Length: 481;
 Best Local Similarity 42.3%; Pred. No. 1.7e-30;
 Matches 91; Conservative 34; Mismatches 69; Indels 21; Gaps 3;
 Qy 1 QSGPLPKPSLQALPSSLVPLEKPTVLRQGPPGVLDYRLEKLSRSSRYQD-----QA 51
 22 QAGPLPKPTIWAEPGSVITWCQSLQVAKPSLSAQPGPAVSSGGVT 81
 Cy 52 VLFIPAMKRSLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGVT 111
 82 RFSIPSMEHAGRVRYCVRSPAGWSEFSDPYLEWVTPGSTPLSALPSWPWASGGNT 141
 Db 112 LQCQTRYGFQFQALYKEGDPAFYKNPER-----WYRASPFITIVTAHSSTYRCYS 162
 142 LRCGSQKGYCHFVLMKEGE---HOLPOTLDSQHLHSGGFOALEFPVGVPWPSHRWFTRCYV 198
 Qy 163 FSSRDPYIANSAPSDPPELWVITGTSVTPSLRPTEP 197
 Cb 199 SYRNTPOVWSHPSDPELEILPSGVSKPSLTLQGP 233
 RN [1]
 RESULT 5
 OBNHG6 PRELIMINARY; PRT; 447 AA.
 ID Q8NHJ6
 AC Q8NHJ6;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor-5.
 GN LIRBS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBITaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Canavez F.C.;
 Rj Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF283988; AAL36992.1; -.
 DR InterPro; IPR00306; Ig_MHC.
 DR Pfam; PF00047; ig; 2.
 KR Receptor.
 SQ SEQUENCE 447 AA; 49193 MW; 6B1E83E2BB107614 CRC64;
 32.1%; Score 419; DB 4; Length 447;
 Best Local Similarity 44.2%; Pred. No. 4.9e-30;
 Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;
 Query Match 32.1%; Score 419; DB 4; Length 447;
 Best Local Similarity 44.2%; Pred. No. 4.9e-30;
 Matches 95; Conservative 27; Mismatches 79; Indels 14; Gaps 2;
 Qy 1 QSGPLPKPSLQALPSSLVPLEKPTVLRQGPPGVLDYRLEKLSRSSRYQD-----QA 51
 22 QAGPLPKPTIWAEPGSVITWCQSLQVAKPSLSAQPGPAVSSGGVT 81
 Cy 52 VLFIPAMKRSLAGRYRCSYONGSLWSLPSDQLELVATGVFAKPSLSAQPGPAVSSGGVT 111
 82 RFSIPSMEHAGRVRYCVRSPAGWSEFSDPYLEWVTPGSTPLSALPSWPWASGGNT 141
 Db 112 LQCQTRYGFQFQALYKEGDPAFYKNPER-----WYRASPFITIVTAHSSTYRCYS 162
 142 LQCQTRYGFQFQALYKEGDPAFYKNPER-----WYRASPFITIVTAHSSTYRCYS 201
 Qy 167 DPYIWSAPS DPLELWVITGTSVTPSLRPTEPSSVA 201
 Db 202 SHYLLSHPSDPELELWVSGSLEGPRPSPTRSVSTA 236
 RN [1]
 RESULT 7
 OBNHLS PRELIMINARY; PRT; 448 AA.
 ID Q8NHLS
 AC Q8NHLS;
 DT 01-OCT-2002 (TREMBLrel. 22, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Leukocyte immunoglobulin-like receptor 5.
 GN LIR5.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CX NCBITaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20395285; PubMed=10941837;

DR InterPro; IPR00710; Ig-like.
 DR InterPro; IPR033598; Ig_c2.
 DR InterPro; IPR033006; Ig_VHC.
 DR SMART; SMC0409; Ig; 4.
 DR SMART; SMC0408; IgC2; 2.
 DR PROSITE; PS50835; Ig_LIKE; 2.
 KW Immunoglobulin domain; Receptor; SEQUENCE; 631 AA; 69456 MW; 10E7B706D234D6EF CRC64;

Query Match 31.9%; Score 415.5; DB 6; Length 631;
 Best Local Similarity 38.1%; Pred. No. 1.6e-29;
 Matches 101; Conservative 44; Mismatches 101; Indels 19; Gaps 6;

Cy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLYRERKLSSRYQD----CA 51
 22 QAGPLPPTIWAEPGSVIRGSPVTIWCQGNLEAQEYRLDKEGSPEPLRNK 81

Db 52 VLFIPAMKSLAGRGRCSYONGSLWSLSPSDQELVALGVFAKPSLSAQPGPAVSSGGDT 111
 82 RFSPIPSNTQHAGRYRCYVRSPAGWSEPSDPLELWVTFYSKPTLSALPSPTVASSGNT 141

Cy 112 LQCQTRYGFDFALYKEGD---PAPYKNEP---RWYRASFPITVTAHSGTYRCYS 165
 142 LRCGSQKGYDHFLVFKGEHQ_PRTLDSQQLHSGGFFQNLFFVGPVTPSHWRFRCVYFT 201

Dy 166 RDPYLWSAPSAPSDPLEWVVTGTSVTSPSRLLPTEPPSSVAESEATAEL---TUSFTNKVFT 223
 202 YNDQWRSHPSSPLELPSGVSRKFSLTJQGP-VLAPGESLTUQCCSDVGYDRFVLYKEG 253

Qy 224 SRSITTSKESDSRAGPARQVYTKG 248
 261 ERDFLURPGQQPQ-AGLSQANFTLG 284

Db 112 LQCQTRYGFDFALYKEGD---PAPYKNEP---RWYRASFPITVTAHSGTYRCYS 162
 142 LQCGSQNAFGGFTLKKEGED---ERHPQCVNSHTLQGWSWAFISVGPVSPSPSRWSYRCG 198

Cy 163 FSSRDPYIWSAPSAPSDPLELWVVTGTSVTSPSRLLPTEPPSSVAESEATAEL---TUSFTNKVFT 220
 199 YDWSSPYVWASLPSGJLEJVPGVSKPS-LSVQGPVVAPEGEILTDQGSDVGYDRFVLY 257

Dy 221 TETRSRITTSKESDSPAGPARQVYTKG 248
 258 KEGERDFLQLPGRGPQ-AGLSQANFTLG 284

Db 015471 PRELIMINARY; PRT; 631 AA.

RESULT 11

ID Q8MJZ5 PRELIMINARY; PRT; 645 AA.

AC Q8MJZ5;

DT 01-OCT-2002 (TREMBLrel. 22, Created)

DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Leukocyte immunoglobulin-like receptor b.

GN LIRE.

OS Pan troglodytes (Chimpanzee).

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

CX NCBi_TaxID=9598;

RN [1]

RP SEQUENCE FROM N.A.

RA Canavez F.C., Young N.T., Guethlein L.A., Rajalingam R., Khakoo S.I.,
 RA Shum B.P., Parham P.;
 RT "Comparison of chimpanzee and human leukocyte Ig-like receptor genes
 reveals framework and rapidly evolving genes.";
 RL J. Immunol. 167:5786-5794(2001).

DR EMBL; AF383166; AAL31875.1; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003598; Ig_c2.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF000734; Lipase.

DR SMART; SMC0407; Ig; 3.

DR PROSITE; PS50835; Ig_LIKE; 1.

DR PROSITE; PS00120; LI_PASE_SER; 1.

DR Receptor; Signal; 1 23 POTENTIAL.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 631 MONOCYTE INHIBITORY RECEPTOR.

SEQUENCE 631 AA; 69386 MW; 61CF1967B308D79FA CRC64;

Query Match 31.1%; Score 405.5; DB 4; Length 631;
 Best Local Similarity 37.0%; Pred. No. 1.3e-28;
 Matches 98; Conservative 40; Mismatches 108; Indels 19; Gaps 6;

Cy 1 QSGPLPKPSLQALPSSLVPLEKPVTLRCQGPGVLYRERKLSSRYQD----CA 51
 22 QAGPLPPTIWAEPGSVIRGSPVTIWCQGSJEAQEYRLDKEGSPEPLRNK 81

Dy 52 VLFIPAMKSLAGRGRCSYONGSLWSLSPSDQELVALGVFAKPSLSAQPGPAVSSGGDT 111
 82 RFSPIPSNTQHAGRYRCYVRSPAGWSEPSDPLELWVTFYSKPTLSALPSPTVASSGNT 141

Cy 112 LQCQTRYGFDFALYKEGD---PAPYKNEP---RWYRASFPITVTAHSGTYRCYS 165
 142 LRCGSQKGYHFVFLVFKGEHQ_PRTLDSQQLHSGGFFQALFPVGPVNPSPHRWRFCYVY 201

Db 166 RDPLWSAPSAPSDPLELWVVTGTSVTSPSRLLPTEPPSSVAESEATAEL---TUSFTNKVFT 223

RESULTS 13

ID Q8SPQ5 PRELIMINARY; PRT; 336 AA.

AC Q8SPQ5; 01-JUN-2002 (TREMBLei). 21, Created)

DT 01-JUN-2002 (TREMBLei). 21, Last sequence update;

DE NK receptor KIR2DL1.

GN Bos taurus (Bovine).

OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

RN .1i - TaxID=9913;

RP SEQUENCE FROM N.A.

RX MEDLINE=21853859; PubMed=11870625;

RA McQueen K.L., Wilhelm B.T., Harden K.J., Mager D.L.; "Evolution of NK receptors: a single Ly49 and multiple KIR genes in the cow"; Eur. J. Immunol. 32:810-817(2002).

DR EMBL; AY0751C2; AAL82801; 1; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR003006; Ig_MHC.

DR Pfam; PF00047; Ig; 2.

DR SMART; SMC0409; Ig; 2.

KW Receptor.

SQ SEQUENCE 336 AA: B4B4B46A5F089D02 CRC64;

Query Match: Best local Similarity 30.8%; Score 401; DB 6; Length 336; Matches 96; Conservative 24; Mismatches 79; Index 14; Gaps 5;

QY 1 QSGPLPKPSLQLPSSVLEPLKPVTLRCQGPPGVDYRERKASSRRYQD-QAVUF---- 54

Db 2 DEGGHDKPSSLAWPSPPWFGQGHTLRCQSPLGPFERFLHKDRTRNPELGGIIFWKFL 81

QY 55 IPAMKRSLAGRYRC--SYCN-GSLWSLPSDQLEJLAVATGVFAKISLSAQPGPAVSSGGDV 111

Db 82 MGPVTEAHAGTYRCHGHYSHLPLNLWSAPSDFPLEWVUIGLSSKKDSISAQGGPVVRSGEV 141

Qy 112 LQCQTRYGFDFQFALYKEG---DPAPYKPNPERWYRASSPPIITVTAHSGTYRCYSFSSR 166

Db 142 LVCSSESAFDQFHILREGVNLGRPLLAGGRGPRCALQAEFPPLGP3;PDHSGVYRCYGSFTR 202

QY 167 DPYLWSAPSDFPLEWVUTGTSV-PSRLPTEPSS 199

Db 202 SPYSWSDSSDFPLIYLSVTGNSSSSQPIHTKNSN 234

RESULTS 14

075022 ID Q75022 PRELIMINARY; PRT; 631 AA.

AC DT 01-NOV-1993 (TREMBLei). 08, Created)

DT 01-NOV-1998 (TREMBLei). 08, Last sequence update;

DT 01-MAR-2003 (TREMBLei). 23, Last annotation update;

DE Leucocyte immunoglobulin-like receptor-3.

GN LIR-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1] SEQUENCE FROM N.A.

RESULTS 15

ID Q8M2Z7 PRELIMINARY; PRT; 643 AA.

AC Q8M2Z7; 01-OCT-2002 (TREMBLei). 22, Created)

DT 01-OCT-2002 (TREMBLei). 22, Last sequence update;

DT 01-MAR-2003 (TREMBLei). 23, Last annotation update;

DE Leukocyte immunoglobulin-like receptor 8.

GN LIR8.

OS Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

OX NCBI_TaxID=9598;

RN [1] SEQUENCE FROM N.A.

RA Borges J., Hsu M.-L., Fanger N., Kubitt M., Costman J.; J. Immunol. 0:0-C(1997); DR EMBL; AF025533; AAB87667.1; -.

DR HSSP; P43626; INKR; InterPro; IPR003599; Ig-like.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR000734; Lipase.

DR Pfam; PF00047; Ig; 3.

DR SMART; SY00409; Ig; 1.

DR PROSITE; PS00120; LIPOASE SER; 1.

DR PROSITE; PS00120; LIPOASE SER; 1.

DR SEQUENCE 631 AA; 69226 MW; E77E1E38D42F9C25 CRC64;

Query Match: Best Local Similarity 30.7%; Score 400.5; DB 4; Length 631; Matches 17; Conservative 43; Mismatches 81; Index 227; Gaps 9;

QY 1 QSGPLPKPSLQLPSSVLEPLKPVTLRCQGPPGVDYRERKASSRRYQD----CA 52

Db 2 QAGPFPKPTLWAEPGSVISWGSTPVTIWCQSLAEQEVQCLDKECSCPEELDRANKRLEPKNA 81

QY 52 VLFIPAKRSLAGRYRCYQNGSLWS;PSDQLEJLAVATGVFAKPSLSAQPGPAVSSGGDV 111

Db 82 RFSIPSWTCHHAGRVRCHYSSAGWSEPSDPLEWVTTGAYSKPTLSA;PSPVWASGGNT 141

QY 112 IQC--QTRY----- 118

Db 142 LRCCGSQKRYH;HFVLMKEGEHQLPRTLDSQQLHSGGFCQALFPVGPNPNSHRWFICYYMM 202

QY 131 -----PAPYKNEPE----- 140

Db 202 NTPRWSHPSCPLEILPSGVSRKPS;LTQGPVLAPGQSI;TQGSDVGYDREFVLYKEGE 261

QY 141 -----PAPYKNEPE----- 145

Db 322 RDFLQRGQQPCAGSQAQNFTLGPVS;SNGQYRCY3AHLISSEWSA2SDPDLNIMAGQI 321

QY 146 PIITVTAHSGTYRCYSFSSRDYPLWAPSDFPLEWVUTGTSVTPSLPTEPSS--VAEF 203

Db 382 PMSPVTSAGHTYRCYGRSSNPYLISHPSPELELWVSGHSGSSLPPGPRSTPGIYR 441

QY 204 SEATAELTVSFTNKVF-----TTETSRSSITSPKESD--SPAGPA 241

Db 442 LEVLIGVSVAFVLLFLFLFLRQRHSHKRTSDQRKTDFCRPAGAA 489

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7

DR InterPro; IPR003599; Ig.
 DR InterPro; IPR003598; Ig- c2 .
 DR InterPro; IPR003366; Ig-MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SMC03409; Ig; 4.
 DR SMART; SMC0408; IgC2; 2.
 KW Immunoglobulin domain; Receptor.
 SEQUENCE 643 AA; 70504 MW; BEBC8F940B5F65AC CRC64;

```

Query Match: 30.7%; Score 430; Dd 6; Length 643;
Best Local Similarity 44.2%; Pred. No. 4.4e-28;
Matches 91; Conservative 27; Mismatches 74; Indels 14; Gaps 2;
Qy 1 QSGPLPKPSLQLALPSSLVPLEKPVTLRCQGPPGVQDYLXRUEKLSSSRYQDQAVLFIPAMKR 60
Qy 22 CAGTLPKPTLWAEPASVIARGKPVTLWCQGPLETEEYRLDKEGLPWAWERQNPLEPGAKA 91
Qy 62 SL-----AGRVRCSYQNGSLMSLPSDQELEJRTGURKAQPSLSAQDGPAVSSGGMT 112
Qy 82 KFHILSTVVDSDSAGRVRYYETPAGWSEPSDPLELVALTGFYAEPTELLALPSPVVAASGGNT 141
Qy 112 TQCQTRYGFDDALYKEGDPAP----YKNPERWYRASFPPIITVTAHSGTYRCYSFSSR 166
Qy 142 LQCDTRDGGLTFVLVEEQKLPRTLYSQKLPKGPSRALFPVGTPSPSRWRFRCCYYYRK 202
Qy 167 DPYLNAPSDDPLELUVVIGTSVTPSRL 192
Qy 202 NNPQWNSHPSSDLIELIVPGVSRKPSLL 227
Db

```

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OM protein - protein search, using sw model

Run on: November 10, 2003, 06:15:04 ; Search time 21 Seconds
(without alignments)
1140.286 Million cell updates/sec

Title: US-09-503-387-9

Perfect score: 1304

Sequence: I QSGPLPKPSLQALPSSLVPL.....SPKESDSPK3PARYTKG 249

Scoring table: BLCSJM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 96158682 residues

Total number of hits satisfying chosen parameters: 283309

Minimum DB seq length: 0

Maximum DB seq length: 20000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_76:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	%	Match Length	DB ID	Description
1	1304	130.0	339	2	JC7509	glycoprotein VI-1
2	381	23.2	466	2	JC5897	killer cell inhibitory cell receptor
3	375	28.8	264	2	JC6020	FC gamma 2 receptor
4	372.5	28.6	841	2	JC5894	killer cell inhibitor
5	365.5	28.0	635	2	JC5896	killer cell inhibitor
6	345.5	26.5	680	2	JC5895	KIR (cl-1) NK rec
7	320.5	24.6	444	2	G01925	cell surface glycoprotein
8	314.5	24.1	296	2	B53434	natural killer cell inhibitor
9	314	24.1	348	2	A56247	natural killer cell inhibitor
10	312.5	24.0	341	2	I61725	KIR (cl-2) NK rec
11	312.5	24.0	444	2	G01924	FcalpharB - human
12	304	23.4	239	2	B53430	cell surface glycoprotein
13	302	23.2	335	2	A53434	IGA (Fc) receptor
14	299	22.9	287	2	JH0332	killer cell inhibitor
15	295.5	22.7	427	2	G02034	KIR (cl-5) NK rec
16	291.5	22.4	455	2	G01923	membrane glycoprotein
17	280	21.5	303	2	A408C7	immunoglobulin-like
18	275.5	21.1	1327	2	T09452	alpha-1-B-glycoprotein
19	145	11.1	237	2	A42013	hypothetical protein
20	142.5	10.9	474	1	OMHJ1B	heparan sulfate proteoglycan
21	141.5	10.9	184	2	T46433	FC-gamma RIIB-alp
22	126.5	9.7	3707	2	S18252	alpha-1-B-glycoprotein
23	124.5	9.5	267	2	I56110	hypothetical protein
24	118.5	9.1	267	2	A35902	receptor
25	115	8.8	283	1	FCMSG1	FC gamma (IgG) rec
26	114.5	8.7	1259	2	A3425	FC gamma (IgG) rec
27	113.5	8.7	1268	1	A3964C	Bravo/Nr-CAM cell adhesion molecule
28	111.5	8.6	4391	2	A38096	neuronal cell adhesion molecule
29	110	8.4	270	2	A34636	perlecan precursor

connectin/titin -
Fc gamma (IgG) rec
Fc gamma (IgG) rec
Fc gamma (IgG) rec
Fc-gamma-1/gamma-2
Fc gamma receptor
duttl protein - mouse
hypothetical protein
IgE Fc receptor alpha
Fc Gamma (IgG) rec
Glucan 1,4-alpha-g
vascular celi adhesin
transmembrane rece
BPLF1 protein - hu
CDC protein - rat

ALIGNMENTS

RESULT 1

JC7509

glycoprotein VI-1 - human

C;Species: Homo sapiens (man)

C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001

C;Accession: JC7509; PC7101

R;Bzumi, Y.; Uchiyama, T.; Takayama, H.

Biochem. Biophys. Res. Commun. 277, 27-36, 2003

A;Title: Molecular cloning, genomic structure, chromosomal localization, and alternative splicing of the human platelet

A;Contents: Platelet

A;Accession: JC75C9

A;Molecule type: mRNA

A;Residues: 1-339 <EZU>

A;Cross-references: PC7101

A;Molecule type: protein

A;Accession: DDBJ:ABC43819

C;Comment: This protein, which belongs to the immunoglobulin superfamily, is the major gamma chain as a signal transducing subunit, and plays some roles in cancer cells

C;Genetics:

A;Gene: gpVI-1

A;Map position: 19q13.4

A;Introns: 52/1; 95/1; 353/1; 638/1; 692/1; 752/1; 803/1

C;Keywords: glycoprotein; immunoglobulin; platelet

Query Match

Best Local Similarity

Matches 249; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Length 339;

Score 100.0%; Pred. No. 2.8e-95;

C;Query

1 QSGPLPKPSLQALPSSLVPLKEPVTLRCQGPQPGDVGDUYREKLSSRYDCAVLPFAMKR

Db 21 QSGPLPKPSLQALPSSLVPLKEPVTLRCQGPQPGDVGDUYREKLSSRYDCAVLPFAMKR

Db 81 SLAGRYRCSYQNGSLSWPSDQLELVATGVFAKPLSQAQGPAGVSSGGDVTLQCTRYGF

QY 62 SLAGRYRCSYQNGSLSWPSDQLELVATGVFAKPLSQAQGPAGVSSGGDVTLQCTRYGF

QY 121 DQFALKYEGDPAPYKNPERWYRASPIITVTAHSGTYRCYSFSSRDFYLWSAPSDFLEL

QY 141 DQFALKYEGDPAPYKNPERWYRASPIITVTAHSGTYRCYSFSSRDFYLWSAPSDFLEL

Db 181 WVTGTSWTPSLRPTEPSSVAESEAELTVSFNKVFTETRSRSTSITSPKESDSPAGP

Db 201 WVTGTSWTPSLRPTEPSSVAESEAELTVSFNKVFTETRSRSTSITSPKESDSPAGP

QY 241 AROYYTKGN 249

Db 261 AROYYTKGN 269

RESULT 2

JC5897

killer cell inhibitory receptor p91 precursor - human

C;Species: Homo sapiens (mar)

C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999

C;Accession: JC5897

R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.; Chya

J. Biochem. 123, 358-368, 1998

A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory

A;Reference number: JC5894; MUID:98218758; PMID:9538215

A;Accession: JC5897

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-466 <YAM>

A;Cross-references: GB:AF041034; NID:g2791689; PID:92791693

C;Comment: This protein function as inhibitory cell-surface molecule against cell activation

C;Genetics:

A;Map position: 19q13.3-13.4

F;1-23/Domain: signal sequence #status predicted <SIG>

Query Match 29.2%; Score 381; DB 2; Length 466;

Best Local Similarity 38.2%; Pred. No. 1.8e-22; Mismatches 104; Indels 24; Gaps 3;

Matches 102; Conservative 37; Mismatches 104; Indels 24; Gaps 3;

QY 1 QSSPLPKPSIQLALPSSIVPLEKPVTLRCQGGPGVD---LYREKLSS--SRYQD---CAV 52

Db 2 CAGHIIPKTLWAEGPSVLIQGSPVTLRCQGLSQASEVILYRENKSASWVRICCPGKNGQ 81

QY 3 LEIPAMKRSLAGRGRCSYQNGSISLPSDQELVATGVFAKPSLSAQGPRAVSSGGDV 112

Db 32 FPIPSITWEHAGRYHCQQYISHNHSSEYSDPLEUWVTGAVSKFTSALPSPVTLGGNVI 142

QY 113 QCCTTRYGFDFALYKEGDPAKYKPERW-----YRASFPPIITVTAHSGTYRCYSF 163

Db 142 QCVSQVAFDGFLIKEGED---EHPORLNHSKARGSSRAIFSVGPGPVSPNRKSHRCGY 198

QY 164 SSRDPYIWSAPSDDPELVTGTSVTPSRILTEPPSSVAEFESEAATELT--VSFTNKVFT 221

Db 199 DLNSPYNWSSPSQELLELLVPGVSKKPS-LSVQPGPVARGESLTLCQVSDVGYDRFVLYK 257

QY 222 ETRSRITTSPKESDSPAGPARQYXTKG 248

Db 258 EGERDIRCLPGRQQ-AGLSQANFTLG 283

RESULT 3

JC5897

FC gamma 2 receptor precursor - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 05-Nov-1999

C;Accession: I46C20; SS3:15

R;Zhang, G.; Young, J.R.; Tregaskes, C.A.; Sopp, P.; Howard, C.J.

J;Immunol. 155, 1534-1541, 1995

A;Title: Identification of a novel class of mammalian FC gamma receptor.

A;Reference number: I46020; MUID:95363119; PMID:7636215

A;Accession: I46020

A;Status: Preliminary; translated from GB/EML/DCBJ

A;Molecule type: mRNA

A;Residues: 1-264 <ZFA>

A;Cross-references: EMBL:Z37506; RID:9732571; PIEN:CLASS5736.1; PID:9732572

C;Keywords: immunoglobulin receptor

Query Match 28.8%; Score 375; DB 2; Length 264;

Best Local Similarity 42.1%; Pred. No. 2.7e-22; Mismatches 85; Conservative 29; Mismatches 68; Indels 20; Gaps 4;

Matches 85; Conservative 29; Mismatches 68; Indels 20; Gaps 4;

QY 1 QSGPUPKPSLQALPSSLVPLEKPVTLRCQGPNGDLYRKLEKSS----RYQDA 51

Db 2 2 QAGTFFPKIWIAPSSVVPGLSSVTILCGGPNTKSFSLNKEGSTPWNHPSLPWDKA 81

QY 52 VLFIPIAMKRSLAGRGRCSYQNGSISLPSDQELVATG-----VFKPSLSAQGPRAV 105

Db 82 MFFISNVREQQAGRYHCSHFGVNWSEPEPDLLVAGEPAGRLDRPSJSVRPSPSVA 141

RESULT 4

JC5894

killer cell inhibitory receptor p91A precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 17-Mar-1999

C;Accession: JC5894

R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.

J. Biochem. 123, 358-368, 1998

A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory

A;Reference number: JC5894; MUID:98218758; PMID:9538215

A;Accession: JC5894

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-841 <YAM>

A;Cross-references: GB:AF040946

C;Comment: This protein function as inhibitory cell-surface molecule against cell activation

C;Genetics:

A;Map position: 7

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-841/Product: killer cell inhibitory receptor p91A #status predicted <MAT>

F;24-118;13-220;221-315;316-418;419-517;518-618/Domain: extracellular Ig-like #status predicted <TM>

F;636-674/Domain: transmembrane #status predicted <TM>

F;675-765/Domain: cytoplasmic #status predicted <CYT>

Query Match 28.6%; Score 372.5; DB 2; Length 341;

Best Local Similarity 38.5%; Pred. No. 1.8e-21; Mismatches 80; Conservative 35; Mismatches 76; Indels 27; Gaps 3;

Matches 80; Conservative 35; Mismatches 76; Indels 27; Gaps 3;

QY 2 SGELPKPSLQALPSLIVPLEKPVTLRCQGPNGDLYRKLEKSSRCQAVL----- 53

Db 220 SGNLQKPTIAEPGSVITSKRAMTIWCQGNLDAEVYFLHNEGSQKTQSTQTLQQPGNKGK 279

QY 54 -FIPAMKRSLAGRGRCSYQNGSISLPSDQELVATGVFA-KPSLSAQGPRAVSSGGDV 110

Db 280 FPIPSMTQHAGGYCYGCGSAWSQPSETLELWVGTIGYEHYKRLSVLPSPVNTAGNM 339

QY 111 TIQCQTRYGFDFALYKEGDPAKYKPERWYRASFPPIITVTAHSGTYRCYSF 164

Db 34 TLMCASDFHYDKFLIKEDKKFGNSLDTEHISSSRQYRALPFIIGPTIPHTGTFRCGYF 399

QY 165 SRDPYIWSAPSDDPELVTGTSVTPSRILTEPPSSVAEFESEAATELT--VSFTNKVFT 192

Db 430 KNAQOLNSVPSDQLQQLISGLSKKPSLL 427

RESULT 5

JC5896

killer cell inhibitory receptor p91C precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 18-Mar-1998 #sequence_revision 18-Mar-1998 #text_change 05-Nov-1999

C;Accession: JC5896

R;Yamashita, Y.; Fukuta, D.; Tsuji, A.; Nagabukuro, A.; Matsuda, Y.; Nishikawa, Y.

J. Biochem. 123, 358-368, 1998

A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory

A;Reference number: JC5894; MUID:98218758; PMID:9538215

A;Accession: JC5896

A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-635 <YAM>

A;Cross-references: GB:AF041036; NID:g2791693; PID:92791693

C;Comment: This protein function as inhibitory cell-surface molecule against cell activation

F;1-23/Domain: signal sequence #status predicted <SIG>

F;24-118;119-220;221-315;316-418;419-517;518-618/Domain: extracellular Ig-like #status

Query Match 28.0%; Score 365.5; DB 2; Length 635;
 Best Local Similarity 37.5%; Pred. No. 4.4e-21;
 Matches 78; Conservative 38; Mismatches 75; Indels 17; Gaps 3;

Qy 2 SGPLPKPSIQLPSSVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVL----- 53
 Db 220 SGNLOKPTIKAEPGSVIAASKRAMTWCQGNLDAEVYFLHNEGSQKTOSTQTLQOFGNKR 279

Cy 54 -FIPAMKRSLAGRYRCSYONGSLWSLPSDOLELVATGVFA--KPSLSAQPGPAVSSGGDV 110
 Db 280 FFLPSVTQOHAGQYRCYCYSAGWSQPSDTLELVNTGIVIYEHYKPRLSVPSPVUTAGNM 339

Qy 111 TLQCQTRYGFDCFALYKEGD----PAPYKNPERWYRASFPITVTAHSGYRCYSFS 164
 Db 340 TLHCASEDFHYKFITKEDKKFGNSLDETEHISSSRCYRALFIIGPTPTHTGTRFCYGF 399

C;Accession: G01925; C;Keywords: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-R;Colonna, M.; Samaridis, J.

A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-R;Reference number: A56247; NID:95232526; PMID:7716543

A;Status: Preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-444 <RES>

A;Cross-references: GB:L41269; NID:9780307; PID:AAA69870.1; RID:9780308

C;Genetics:

A;Gene: NKAT-3

A;Map Position: 19

Query Match 24.6%; Score 320.5; DB 2; Length 444;
 Best Local Similarity 38.6%; Pred. No. 9.9e-18;
 Matches 83; Conservative 22; Mismatches 81; Indels 29; Gaps 5;

Qy 7 KPSLQALPSSVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVL-----LFI 55
 Db 123 KPSLLAHPGPVLVKSCSERVILQWSDIMFEHHFLKEGISKDPSRLVQGQIHDCGVSKANFSI 182

C;Accession: JCS5895
 J;Biocat. 123, 358-368, 1998
 A;Title: Genomic structures and chromosomal location of p91, a novel murine regulatory protein
 A;Reference number: JCS5894; MUID:98218758; PMID:9538215

A;Accession: JCS5895
 A;Status: nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: -680 <YAY>

C;Cross-references:

C;Comment: This protein function as inhibitory cell-surface molecule against cell activation

C;Genetics:

A;Map Position: 7

F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-118,119-220,221-315,316-418,419-517,518-618/Domain: extracellular Ig-like #status F
 F;636-674/Domain: transmembrane #status predicted <TM>
 F;675-630/Domain: cytoplasmic #status predicted <Cyt>

Query Match 26.5%; Score 345.5; DB 2; Length 630;
 Best Local Similarity 35.1%; Pred. No. 1.8e-19;
 Matches 75; Conservative 39; Mismatches 77; Indels 27; Gaps 3;

Qy 2 SGPLPKPSIQLPSSVPLEKPVTLRCQGPGVLDYRLEKLSSRYQDQAVL----- 53
 Db 220 SGNLOKPTIKAEPGSVIAASKRAMTWCQGNLDAEVYFLHNEGSQKTOSTQTLQOFGNKR 279

Cy 54 -FIPAMKRSLAGRYRCSYONGSLWSLPSDOLELVATGVFA-KPSLSAQPGPAVSSGGDV 110
 Db 280 FFLPSVTQOHAGQYRCYCYSAGWSQPSDTLELVNTGIVIYEHYKPRLSVPSPVUTAGNM 339

C;Accession: B53434
 A;Status: preliminary

A;Molecule type: DNA; mRNA

A;Residues: 1-296 <CDS>

A;Cross-references: GB:JCS5265; NID:9475446; PID:AAA17798.1; SID:9475448; GS:U05266;

C;Genetics:

A;Gene: gp49B

A;Introns: 12/3; 24/2; 119/2; 220/1; 232/1; 249/3; 272/1

C;Keywords: alternative splicing; glycoprotein

Query Match 24.1%; Score 314.5; DB 2; Length 296;
 Best Local Similarity 35.5%; Pred. No. 1.8e-17;
 Matches 81; Conservative 33; Mismatches 93; Indels 21; Gaps 5;

Qy 1 QSGPLPKPSIQLPSSVPLEKPVTLRCQGPGVLDYRLEKLSSRYQD-----CA 51
 Db 22 QAGHLPKPKIWAEPGSVIAAYTSVITWCQGSWEAQYYHYKEKSVPNPWDTCVPLERTKA 61

C;Species: Homo sapiens (man)

C;Accession: G01925; 161726; R;Wagtmann, N.
 submitted to the EMBL Data library, June 1995

Db	Query	Matches	Score	Conservative	Mismatches	Length	Indels	Gaps
Db	142 FSCSSSIVFGRFILIQEGKHGLSWLDSQHQANQPSY-ATFVLDATPHEHNGTFRCGY 199	7	KPSLQALPSSLVPLEKPVTLRCQGPPGVLDLYRLEKLSSRYQD-----QAVL	QY	164 SSRDPYIWSAPSDDPELVLVTGTSVTPSRPTEPPSSVAEF-SEATAEL 210	28 KPSLIAHPGPJMKSEETVILQCSWSDVRFOHFLJHR--EGKFKDTHJIGEHEDGVSKAF 85	Db	A56247? natural killer cell-associated protein - human
Db	200 ERNEPQVWSKPSNLDLMISETK-DQSSTPTEDDASVQNTQSENNAEJ 246	54 FIPAMKRSIAGRYRC-----SYQNGSLWSLPSQJELVATGVEAKPSLSAQPGPAVSS	QY	C;Species: Homo sapiens (man)	142 GESVTLSCSSRSSVWYHLSREGEEAHERRFSAGPKUNGTT-FQADPL-GPATHGTYR 197	66 SIGPMQDLAGTYRCVGSVTHSPYQ---SAPSDDPJDIDIVTGLVKEPKPSLSAQPGPTVLA 141	Db	C;Date: 26-Jul-1995 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999
Db	R;Colonna, M.; Samardis, J.	107 CGDVTRQOCOTRYGFQFALYKEGD-----PAPYKNPERWYRASFPITVTAHSGTYR 159	QY	A;Accession: A56247	142 GESVTLSCSSRSSVWYHLSREGEEAHERRFSAGPKUNGTT-FQADPL-GPATHGTYR 197	160 CYSFSSRDPYIWSAPSDDPELVLVTGTSVTPSRPTEPPS 198	Db	Science 268, 405-408, 1995
Db	A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B	198 QFGSFRRDSDPVEWNNSDPLLVSVTGNPNSWPSPTEPSS 236	QY	A;Reference number: A56247; MID:95232526; PMID:7716543	A;Map position: 19	RESLT 9	Db	A;Status: preliminary; translated from GB/EMBL/DCB
Db	A;Molecule type: mRNA	Query Match 24.1%; Score 314; DB 2; Length 348;	QY	A;Residues: 1-348 <RES>	Best Local Similarity 32.3%; Pred. No. 2.4e-17;	Matches 93; Conservative 36; Mismatches 105; Indels 54; Gaps 10;	Db	C;Genetics:
Db	28 KPSLIAHPGPFLVKSEETVILQCSWSDVMFEEHFLJHR--EGMFNDTLRLIGEHEDGVSKAF 85	QY	7 KPSLQALPSSLVPLEKPVTLRCQGPPGVLDLYRLEKLSSRYQD-----QAVL 53	QY	54 FIPAMKRSIAGRYRC-----SYQNGSLWSLPSQJELVATGVEAKPSLSAQPGPAVSS	Db	A;Gene: GDB:NKAT1	
Db	96 SISRMTOQLAGTYRCVGSVTHSPYQ---VSAPSDDPLDIVIGLYKEPKPSLSAQPGPTVLA 241	QY	107 GGDVTLQCCQTRYGFDOFALYKEGDPAKYKNP----ERWYRASFPITVTAHSGTYRCY 161	QY	107 GGDVTLQCCQTRYGFDOFALYKEGDPAKYKNP----ERWYRASFPITVTAHSGTYRCY 161	Db	A;Cross-references: GDB:NKAT1	
Db	142 GENVTISSLSSRSSYDMYHSREGEEAHERRFLPAGPKVNCTFOADFPL-GPATHGTYRCF 199	QY	162 SFSSRDPYIWSAPSDDPELVLVTGTSVTPSRPTEPPSSVA----EFSEATAELTVSF-- 214	QY	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	Db	A;Cross-references: GDB:NKAT1	
Db	215 -----TNK----VFTTETRSITSPKESDSPAGPARQYVTKGN 249	QY	260 LFFLIIHRWCNSKKNAAVMQDQEASNRTANSESD-EQDPOEVUTQLN 305	QY	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	Db	A;Status: preliminary; translated from GB/EMBL/DDJB	
Db	RESULT 10	Query Match 24.0%; Score 312.5; DB 2; Length 444;	QY	215 -----TNK----VFTTETRSITSPKESDSPAGPARQYVTKGN 249	Best Local Similarity 38.1%; Pred. No. 4.2e-17;	Matches 82; Conservative 22; Mismatches 82; Indels 29; Gaps 5;	Db	A;Molecule type: mRNA
Db	161725 natural killer associated transcript 2 - human	260 LFFLIIHRWCNSKKNAAVMQDQEASNRTANSESD-EQDPOEVUTQLN 305	QY	260 LFFLIIHRWCNSKKNAAVMQDQEASNRTANSESD-EQDPOEVUTQLN 305	Db	A;Accession: 161725		
Db	C;Species: Homo sapiens (man)	Query Match 24.0%; Score 312.5; DB 2; Length 444;	QY	260 LFFLIIHRWCNSKKNAAVMQDQEASNRTANSESD-EQDPOEVUTQLN 305	Best Local Similarity 38.1%; Pred. No. 4.2e-17;	Matches 82; Conservative 22; Mismatches 82; Indels 29; Gaps 5;	Db	C;Accession: 161725
Db	C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 05-Nov-1999	260 LFFLIIHRWCNSKKNAAVMQDQEASNRTANSESD-EQDPOEVUTQLN 305	QY	260 LFFLIIHRWCNSKKNAAVMQDQEASNRTANSESD-EQDPOEVUTQLN 305	Db	R;Colonna, M.; Samardis, J.		
Db	Science 268, 405-408, 1995	123 KPSLIAHPGPFLVKSERVILQCSWSDVMFEEHFLHKEGISKDPSSLVQGOIHDGVSXKANFSI 182	QY	A;Title: Cloning of immunoglobulin-superfamily members associated with HLA-C and HLA-B	161725 natural killer associated transcript 2 - human	RESLT 10	Db	A;Status: preliminary; translated from GB/EMBL/DDJB
Db	A;Residues: 1-341 <RES>	56 PAMKRSIAGRYRC-----SYQNGSLWSLPSQJELVATGVEAKPSLSAQPGPAVSSG	QY	A;Reference number: A56247; MID:95232526; PMID:7716543	161725 natural killer associated transcript 2 - human	183 GPMLIAGTYRCVGSVTHSPYQ---LSAPSDDPLDIVIGPYEKPSLSAQPGPKVQAGE 238	Db	A;Accession: 161725
Db	A;Cross-references: GB:L41268; NID:970305; PIDN: AAC23725.1; PID:9973406	109 DVTIQCOTRYGFDOFALYKEGDPAKYKNP----ERWYRASFPITVTAHSGTYRCYF 163	QY	A;Gene: NKAT1	161725 natural killer associated transcript 2 - human	239 SVTLCSSRSSYDMYHSREGEEAHERRFLPAGPKVNCTFOADFPL-GPATHGTYRCFGS 296	Db	C;Genetics:
Db	A;Molecule type: mRNA	164 SSRDPYIWSAPSDDPELVLVTGTSVTPSRPTEPPS 198	QY	A;Status: preliminary; translated from GB/EMBL/DDJB	161725 natural killer associated transcript 2 - human	297 FRHSPYEWWSKSSDPLVSVTGNPSSWPS2TEPSS 331	Db	C;Accession: 161725
Db	C;Genetics:	RESLT 11	QY	A;Gene: NKAT-2	161725 natural killer associated transcript 2 - human	RESLT 12	Db	Query Match 24.0%; Score 312.5; DB 2; Length 341;
Db	Best Local Similarity 37.4%; Pred. No. 3.1e-17;	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	QY	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	Db	Query Match 24.0%; Score 312.5; DB 2; Length 341;		
Db	R;var Dijk, T.B.; Morton, H.C.; Caldenhoven, E.; Bracke, M.; Raaijmakers, J.A.M.; Lam	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	QY	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	Db	Query Match 24.0%; Score 312.5; DB 2; Length 341;		
Db	C;Accession: G02630	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	QY	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	Db	Query Match 24.0%; Score 312.5; DB 2; Length 341;		
Db	C;Species: Homo sapiens (man)	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	QY	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	Db	Query Match 24.0%; Score 312.5; DB 2; Length 341;		
Db	C;Date: 21-Dec-1997 #sequence_revision 06-Jun-1997 #text_change 17-Jul-1998	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	QY	200 GSPHDSPYEWWSKSSDPLVSVTGNPNSWPSPTESKTNFRHLHILIGTSWVILFI 259	Db	Query Match 24.0%; Score 312.5; DB 2; Length 341;		

Matches 77; Conservative 21; Mismatches 74; Indels 29; Gaps 5;
 Qy 7 KPSLQAIKPSLILVPIEKPVTLRCQGPPGVLYRLEKLSSRYQDQAV-----LFI 55
 Db 123 KPSLLAHKPGPLVKSGERVLQILOQWSDIMFEHFFLUHKEGISKDPSRLVQGIHDGVSKANFSI 182
 Qy 56 PAMKRSLAGRYRC-----SYQNGSLWLSIPLSDQLELVATGVFAKPSLSACPGPAVSSG 108
 Db 193 GPMMLALAGTYRCYGSVTHTPYQ----SAPSPLDIVTGPYKEPKSLSAOPGPKVOAGE 235
 Qy 109 DVTIQCCTRYGFDOALYKEGDPAPYKNP-----ERWYRASFPITVTAHSGYRCYSE 163
 Db 239 SVTRISCSSRSSYDMLHSRERRAHLRUPAVRKVNRTFOADFL--GPATHGTYRCFGS 296
 Qy 164 SSRDPYIJKSAPSDDPSELVVTG 184
 Db 297 FRESPPVENSOPSDPLLVSVTG 317

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